

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: May 24, 2002, 19:15:39 ; Search time 1997.16 Seconds

(without alignments)
3981.696 Million cell updates/sec

Title: W36511
Perfect score: 380
Sequence: 1 GCAGGCGACGCTGCTCC.....ACTATTATTACCAATGAC 380

- Scoring table:
IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 segs, 10463268293 residues
Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
GenBankl : *
1: gb_da : *
2: gb_htg : *
3: gb_in : *
4: gb_om : *
5: gb_ov : *
6: gb_pat : *
7: gb_ph : *
8: gb_pl : *
9: gb_pr : *
10: gb_ro : *
11: gb_sts : *
12: gb_sy : *
13: gb_un : *
14: gb_vl : *
15: em_da : *
16: em_fun : *
17: em_hum : *
18: em_in : *
19: em_mu : *
20: em_om : *
21: em_or : *
22: em_ov : *
23: em_pat : *
24: em_ph : *
25: em_pl : *
26: em_ro : *
27: em_sts : *
28: em_un : *
29: em_vl : *
30: em_htg_hum : *
31: em_htg_inv : *
32: em_htg_other : *
33: em_htgo_inv : *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Query Match Length DB ID Description

1	186.8	49.2	2347	10	MMY14334	Y14334 Mus musculus
2	185.2	48.7	2225	10	AF059251	AF059251 Mus musculus
3	166.4	43.8	183759	2	AL645902	AL645902 Mus musculus
4	166.4	43.8	261031	2	AL645527	AL645527 Mus musculus
5	135.8	35.7	2278	2	AF059250	AF059250 Homo sapi
6	135.8	35.7	2469	6	AR106047	AR106047 Sequence
7	135.8	35.7	2469	6	AF038461	AF038461 Homo sapi
8	121.6	32.0	13652	9	HSA305027	HSA305027 Homo sapi
9	121.6	32.0	159582	2	AC015734	AC015734 Homo sapi
10	102.4	26.9	3636	10	MMN18477	MMN18477 Mus musculus
11	57.4	15.1	4293	9	HSA305021	HSA305021 Homo sapi
12	57.4	15.1	36006	2	AC107913	AC107913 Homo sapi
13	57.4	15.1	159582	2	AC015734	AC015734 Homo sapi
14	55.2	14.5	2136	6	AX304470	AX304470 Sequence
15	55.2	14.5	3082	6	AF182218	AF182218 Homo sapi
16	55.2	14.5	3362	10	HSA269499	HSA269499 Homo sapi
17	50.6	13.3	2536	10	MMALOXE3	MMALOXE3 Mus musculus
18	50.6	13.3	2685	6	AR142985	AR142985 Sequence
19	50.6	13.2	2685	6	HSU78294	HSU78294 Homo sapien
20	50.6	13.2	2942	10	BC015253	BC015253 Mus musculus
21	50.6	13.2	3203	10	MMALOXE3	MMALOXE3 Mus musculus
22	50.6	13.2	3205	6	AR142986	AR142986 Sequence
23	50.6	13.2	3205	10	MMO93277	MMO93277 Mus musculus
24	49.4	13.0	2826	2	HSA305031	HSA305031 Homo sapi
25	49.4	13.0	36006	2	AC107913	AC107913 Homo sapi
26	48.4	12.7	1944	9	AF468052	AF468052 Homo sapi
27	48.4	12.7	2031	9	AF468051	AF468051 Homo sapi
28	48.4	12.7	2111	2	AF468054	AF468054 Homo sapi
29	48.4	12.7	261031	2	AL645527	AL645527 Homo sapi
30	48.4	12.6	2101	4	AF107263	AF107263 Bos taurus
31	45	11.8	2335	9	HUMLEPXYG	M58704 Human cell
32	45	11.8	2344	9	HUMLEPXYG	M58704 Human cell
33	45	11.8	2344	9	HUMLEPXYG	M58704 Human cell
34	44	11.6	1580	9	AF149095	AF149095 Homo sapi
35	44	11.6	1809	9	AF468053	AF468053 Homo sapi
36	42.6	11.2	15898	1	AX024393	AX024393 Sequence
37	42.6	11.2	15898	6	AX024286	AX024286 Sequence
38	42	11.1	173878	2	AC040977	AC040977 Homo sapi
39	42	11.1	220399	2	AC015918	AC015918 Homo sapi
40	37.4	9.8	148159	2	AC084327	AC084327 Mus muscu
41	36.4	9.6	274656	2	AC079538	AC079538 Mus muscu
42	36.2	9.5	120240	2	AC097176	AC097176 Oryza sat
43	35.2	9.3	1819	6	AX098513	AX098513 Sequence
44	35	9.2	1665	4	BT12LIP0X	Y08829 B. laurus mr
45	34.8	9.2	40172	2	AC017567	AC017567 Drosophila

ALIGNMENTS

RESULT 1
LOCUS MMY14334 2347 bp mRNA linear ROD 11-MAR-1999
DEFINITION Mus musculus mRNA for arachidonate 12-lipoxygenase, 12R-type.
ACCESSION Y14334
VERSION Y14334.1 GI:3043452
KEYWORDS 12(R)-lipoxygenase; Alox12B gene; arachidonate 12-lipoxygenase.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 2347)
AUTHORS Krieg, P.
TITLE Direct Submission
JOURNAL Submitted (28-JUL-1997) P. Krieg, German Cancer Research Center, Research Program 2, Im Neuenheimer Feld 280, D-69120 Heidelberg, Germany, FRG
REMARK 2 (bases 1 to 2347)
REFERENCE 2 (bases 1 to 2347)
AUTHORS Krieg, P., Kinzigt, A., Heldt, M., Marks, F., and Furstenberger, G.
TITLE cDNA cloning of a 8-lipoxygenase and a novel epidermis-type lipoxygenase from phorbol ester-treated mouse skin
JOURNAL Blochim. Biophys. Acta 1391 (1), 7-12 (1998)

MEDLINE 98186642
 3 (bases 1 to 2347)
 REFERENCE Kriegl, P., Siebert, M., Kinzig, A., Marks, F., and Fuerstenberger, G.
 AUTHORS Murine 12(R)-lipoxigenase: functional expression, genomic structure
 TITLE and chromosomal localization
 JOURNAL Unpublished
 FEATURES Location/Qualifiers
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 /organism="Mus musculus"
 /strain="NMRI"
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 /clone_lib="TPA-treated epidermis cDNA in lambda ZAPIT"
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 /gene="Alox12b"
 176..2281
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 LAFLKGIYDRKRSKRLKIDINIPATSVSEVYAEHMTDSFEGYGLNGINGL
 IIRCTQIPDKRPVTDENVAPELGGSTLQALELNGNLYADRIIDGIPTELNGOO
 HHCAAPMLHFGPDGNMFIATIQSLTPEDPDPILPNDEMDLLAKTWVYAEFS
 HEVAHLLESHLIGEAFCIALRLNPMCHPLKLIPIHTRYNVOINSIGRALINKG
 LSARMSLIGLGEFAQVAVRGLSELTYKSLIPNDYFVRGVODLPGYFERDSLAWIA
 MERYVTETIYYYPNDAAVEGDPQLQVOEIFKELCLRESSGEPICLRTIPELLEY
 VTMWYTSARHAHVNSQLEYSMPNPFSSMRNPPMOTKGLTTLQTYMDTLDPVKT
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 BASE COUNT
 ORIGIN
 polyA-site
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 Best Local Similarity 98.5%; Pred. No. 1.9e-36;
 Matches 199; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
 175 TTTCCTGGGCTAGAGGGCTTCGACAGGTGATGTTGGGGGTCTGTGAGCTCAGCT 234
 1542 TGTCCCTGGGCTAGAGGGCTTCGACAGGTGATGTTGGGGGTCTGTGAGCTCAGCT 1601
 Db 1542 TGTCCCTGGGCTAGAGGGCTTCGACAGGTGATGTTGGGGGTCTGTGAGCTCAGCT 1601
 QY 235 ACAAAAGCCTGCTGATTCACAGCACTTTGTGAGCGCGGGGTCTCAGAGCTGCTGGGT 294
 Db 1602 ACAAAAGCCTGCTGATTCACAGCACTTTGTGAGCGCGGGGTCTCAGAGCTGCTGGGT 1661
 QY 295 ATTATTTCCGATGACAGCGCTGGCGGTGTGACCGGATGAGAGGTACGTGAC 354
 Db 1662 ATTATTTCCGATGACAGCGCTGGCGGTGTGACCGGATGAGAGGTACGTGAC 354
 QY 355 ATCATCACTTATTTATACCAA 376
 Db 1721 ATCATCACTTATTTATACCAA 1742
 RESULT 2
 AF059251 2225 bp mRNA linear ROD 27-NOV-1998
 LOCUS AF059251 Mus musculus lipoxygenase (alox) mRNA, complete cds.
 ACCESSION AF059251
 VERSION AF059251.1 GI:3928784
 KEYWORDS

SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 2225)
 AUTHORS Sun, D., McDonnell, M., Chen, X.S., Lakkis, M.M., Li, H., Isaacs, S.N.,
 Human 12(R)-lipoxygenase and the mouse ortholog. Molecular cloning,
 expression, and gene chromosomal assignment
 J. Biol. Chem. 273 (50), 33540-33547 (1998)
 JOURNAL 2 (bases 1 to 2225)
 MEDLINE Sun, D. and Funk, C.D.
 REFERENCE Direct Submission
 AUTHORS Submitted (13-APR-1998) Pharmacology, University of Pennsylvania,
 TITLE 422 Curie Blvd., Philadelphia, PA 19104, USA
 JOURNAL
 FEATURES Location/Qualifiers
 source 1..2225
 /organism="Mus musculus"
 /strain="B6 SJL/J"
 /db_xref="taxon:10090"
 /tissue_type="whole body"
 /dev_stage="newborn"
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 /gene="alox"
 1..53
 /gene="alox"
 54..2159
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 SYHPRRCRNPENPDGYTPGPILINIKATPELNSLRFSVKTSFRLGPMAL
 LAFLKGIYDRKRSKRLKIDINIPATSVSEVYAEHMTDSFEGYGLNGINGL
 IIRCTQIPDKRPVTDENVAPELGGSTLQALELNGNLYADRIIDGIPTELNGOO
 HHCAAPMLHFGPDGNMFIATIQSLTPEDPDPILPNDEMDLLAKTWVYAEFS
 HEVAHLLESHLIGEAFCIALRLNPMCHPLKLIPIHTRYNVOINSIGRALINKG
 LSARMSLIGLGEFAQVAVRGLSELTYKSLIPNDYFVRGVODLPGYFERDSLAWIA
 MERYVTETIYYYPNDAAVEGDPQLQVOEIFKELCLRESSGEPICLRTIPELLEY
 VTMWYTSARHAHVNSQLEYSMPNPFSSMRNPPMOTKGLTTLQTYMDTLDPVKT
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 503 a 647 c 565 g 510 t
 BASE COUNT
 ORIGIN
 3'UTR
 Query Match 48.7%; Score 185.2; DB 10; Length 2225;
 Best Local Similarity 98.0%; Pred. No. 4.8e-36;
 Matches 198; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
 175 TTTCCTGGGCTAGAGGGCTTCGACAGGTGATGTTGGGGGTCTGTGAGCTCAGCT 234
 Db 1420 TGTCCCTGGGCTAGAGGGCTTCGACAGGTGATGTTGGGGGTCTGTGAGCTCAGCT 1479
 QY 235 ACAAAAGCCTGCTGATTCACAGCACTTTGTGAGCGCGGGGTCTCAGAGCTGCTGGGT 294
 Db 1480 ACAAAAGCCTGCTGATTCACAGCACTTTGTGAGCGCGGGGTCTCAGAGCTGCTGGGT 1539
 QY 295 ATTATTTCCGATGACAGCGCTGGCGGTGTGACCGGATGAGAGGTACGTGAC 354
 Db 1540 ATTATTTCCGATGACAGCGCTGGCGGTGTGACCGGATGAGAGGTACGTGAC 354
 QY 355 ATCATCACTTATTTATACCAA 376
 Db 1599 ATCATCACTTATTTATACCAA 1620

RESULT 3
AL645902 183759 bp DNA linear HTG 18-DEC-2001
LOCUS Mus musculus chromosome 11 clone RP23-1912, *** SEQUENCING IN
DEFINITION
ACCESSION AL645902.5 GI:17903578
VERSION HTG; HTGS_PHASE2; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP.
KEYWORDS house mouse.
SOURCE Mus musculus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (sites)
REFERENCE Direct Submission
AUTHORS Lovell, J.
TITLE Submitted (17-DEC-2001) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquerry@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Dec 18, 2001 this sequence version replaced gi:17736621.
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquerry@sanger.ac.uk
----- Project Information
Center project name: BM1912

----- Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid: L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 183739 bases at least Q40
Consensus quality: 183750 bases at least Q30
Consensus quality: 183756 bases at least Q20
Insert size: 190781; 2.6% error; agarose-fp
Insert size: 190781; 2.6% error; agarose-fp
Quality coverage: 17.34x in Q20 bases; sum-of-contigs Quality
coverage: 16.70x in Q20 bases; agarose-fp

* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.

FEATURES

source
1. 183759
/organism="Mus musculus"
/db_xref="taxon:10090"
/chromosome="11"
/clone="RP23-1912"
/clone_1lb="RP23-1912"
1. 183759
/note="assembly-fragment:02187
clone_end:17
vector_side:right"
BASE COUNT 45953 a 44588 c 44502 g 48716 t
ORIGIN

Query Match 43.8%; Score 166.4; DB 2; Length 183759;
Best Local Similarity 99.4%; Pred. No. 1.1e-11;
Matches 167; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 175 TTTCCTGGGCTAGAGGCTGCACAGGTGATGGTGGGGTCTGTGACCTACCT 234
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Db 182008 TGTCCCTGGGCTAGAGGCTGCACAGGTGATGGTGGGGTCTGTGACCTACCT 182067
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QY 235 ACAAGAGCTCTGCATCCCAAGACTTTGTGAGCGCGGGTCCAGAGACTGCTGGG 294
|
Db 182068 ACAAGAGCTCTGCATCCCAAGACTTTGTGAGCGCGGGTCCAGAGACTGCTGGG 182127
|
QY 295 ATATTTCCTGATGAGCGCTGGCGTGTGATGACCGATGAGAGAGCT 342
|
Db 182128 ATATTTCCTGATGAGCGCTGGCGTGTGATGACCGATGAGAGAGCT 182175
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RESULT 4
AL645527 261031 bp DNA linear HTG 30-JAN-2002
LOCUS Mus musculus chromosome 11 clone RP23-26L6, *** SEQUENCING IN
DEFINITION
ACCESSION AL645527.12 GI:18250551
VERSION HTG; HTGS_PHASE1; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP.
KEYWORDS house mouse.
SOURCE Mus musculus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (sites)
REFERENCE Direct Submission
AUTHORS Ashwell, R.
TITLE Submitted (23-JAN-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquerry@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Jan 19, 2002 this sequence version replaced gi:18152591.
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquerry@sanger.ac.uk
----- Project Information
Center project name: BM26L6

----- Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid: L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 257475 bases at least Q40
Consensus quality: 258163 bases at least Q30
Consensus quality: 258659 bases at least Q20
Insert size: 259851; sum-of-contigs
Insert size: 221534; 8.6% error; agarose-fp
Quality coverage: 8.13x in Q20 bases; sum-of-contigs Quality
coverage: 9.54x in Q20 bases; agarose-fp

* NOTE: This is a 'working draft' sequence.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

FEATURES

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/chromosome="11"
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5083. 18204
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18305. 39028
/note="assembly-fragment:04453
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39129. 52548
/note="assembly-fragment:01279
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52649. 83705
/note="assembly-fragment:05674
fragment_chain:1"
83806. 116048
/note="assembly-fragment:02464
fragment_chain:1"
116149. 141576
/note="assembly-fragment:00058
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141677. 170088
/note="assembly-fragment:02429
fragment_chain:1"

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Best Local Similarity	99.4%;	Pred. No. 1.1e+31;		
Matches 167;	Conservative	0;	Mismatches 1;	Indels 0;
				Gaps 0;

LOCUS	DEFINITION	ACCESSION	VERSION	RESULT
AF059250	2278 bp	AF059250	AF059250.1	5
	mRNA	Homo sapiens lipoxxygenase (ALOX12n)	GI:3928782	
	linear	complete cds.		
	PR1			27-NOV-1991

1 (bases 1 to 2278) Sun, D., McConnell, M., Chen, X.S., Lakkis, M.M., Li, H., Isaacs, S.N.,

MEDLINE
9905/919
2 (bases 1 to 2278)
REFERENCE
Sun, D. and Funk, C.D.
TITLES
Direct Submission
JOURNAL
Submitted (13-APR-1998) Pharmacology, University of Pennsylvania,
Philadelphia, PA 19104, USA

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/organism="Homo sapiens"  
/db_xref="taxon:9606"  
/chromosome="17"  
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) at> root 15C"
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5'UTR    1..38
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CDS      38..2143

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Best Local Similarity	83.4%;	Pred. No. 1e-23;		
Matches 166;	Conservative	0;	Mismatches 32;	Indels 1;
				Gaps 1;

RESULT	6		
ARI06047			
LOCUS	ARI06047	2469 bp	DNA
DEFINITION	Sequence 1 from patent US 6103496.		linear
			PAT 14-FEB-200

source	1. .2469	/organism="unknown"
BASE COUNT	522 a	808 c 648 g 491 t
ORIGIN		

Query Match	35.7%	Score 135.8;	DB 6;	Length 2469;
Best Local Similarity	83.4%;	Pred. No. 1e-23;		
Matches 166; Conservative	0;	Mismatches 32;	Indels 1;	Gaps 1
QY	175	TTTCCCTGGGCGCTAGAGCGCTTGGACACAGGATGCTTGGCGGCTCTGAGCTACACT	234	
DB	1626	TGTCCCTGGGCGCTGAGAGCGCTTCTCTGGGCTGATGATGATGACGGGCTCTTCGAGAGTCACT	1685	

QY	233	ACAAAAGCCCTGCACTTCCCAACAGACTTGTGTGAGAGCGCGGGGCCAGAGACCTGCCCTGGGT	294
Db	1686	ATGACAGCCCTACTACTCCCCATGACTTGTGTGAGAGCGTGGGGTCCAGAGACCTGCCCTGAT	1745
QY	295	ATTATTTCGTATGACAGACCTGGGGGTGTGTAGCGATGTGAGAGTACGTGACGTACGAG	354
Db	1746	ATTACTACCGCATGACACACTTGGCGGTGTGTGATGACTCTGGAGAGTATGTGAC-GGAG	1804
QY	355	ATCATCACTTATTATTACC	373
Db	1805	ATCATCACTTATTATTACC	1823

RESULT	7			PRI 16-JUN-1998
*AF038461				
LOCUS	AF038461	2469 bp	mRNA	linear
DEFINITION	Homo sapiens 12R-1ipoxygenase mRNA, complete cds.			
ACCESSION	AF038461			
VERSION	AF038461.1	GI:3220165		
KEYWORDS				
SOURCE	human.			
ORGANISM	Homo sapiens			

REFERENCE	1 (bases 1 to 2469)
AUTHORS	Boeglin,W.E., Kim,R.B. and Brash,A.R.
TITLE	A 12R-11poxygenase in human skin: mechanistic evidence, molecular cloning, and expression
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 95 (12), 6744-6749 (1998)
MEDLINE	98284002
REFERENCE	2 (bases 1 to 2469)
AUTHORS	Boeglin,W.E., Jisaka,M., Kim,R.B. and Brash,A.R.
TITLE	Direct Submission
JOURNAL	Submitted (14-DEC-1997) Clinical Pharmacology, Vanderbilt University, MRB1 RM510, 23rd Ave S. at Pierce, Nashville, TN 37232-6602, USA
FEATURES	Location/Qualifiers
SOURCE	1..2469

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CDS
/cell_type="keratinocyte"
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260..2365
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(12R-hydroperoxyeicosatetraenoic acid)"

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BASE COUNT	522 a	808 c	648 g	491 t
ORIGIN				

[illegible]

Db	1626	TGTCCCTGGGGGTGGAAAGCCTTTGCTGGGGTGTAGTACAGGCGCTCTGTGGAGCTCACT	1685
Oy	235	ACAAAAGCCTCTGCATTTGCCAACAGCATTTGTGGAGCGCGGGTCCAGACCTGCCGTGGT	294
Db	1686	ATGAGAGCCTCTACTCTCCCAATGACTTTGTGGAGCCGTGGGGTCCAGAGCCTGCCTTGAT	1745
Oy	295	ATTATTCCGTGATGACAGCCTGGCGGGTGTGTACGCATATGAGAGTACTGACTAGAG	354
Db	1746	ATTACTACCGGATGACAGCTGGCGGGTGTGTAATGCACGTGAGAGATGTGTGAC -GGAG	1804
Oy	355	ATCATCACTTATTATTACC	373
Db	1805	ATCATCACTTATTATTACC	1823

RESULT	8
LOCUS	HSA305027
DEFINITION	Homo sapiens partial ALOX12B gene for arachidonate 12R-lipoxygenase, exons 3 to 14 and partial ALOX15P pseudogene for arachidonate 15-lipoxygenase, exons 11 to 14.
ACCESSION	AJ305027
VERSION	AJ305027.1 GI:13374920
KEYWORDS	ALOX12B gene; ALOX15P pseudogene; arachidonate 12R-lipoxygenase; arachidonate 15-lipoxygenase.
SOURCE	human.
ORGANISM	Homo sapiens

REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
Direct Submission
Submitted (18-AUG-2000) Krieg P.R., Research Program on Tumor Cell

REMARK	COMMENT	FEATURES
Revised by author 12-MAR-2000	Related sequences: AJ305020 to AJ305031. Overlapping sequences: AC015734, AF163790, AF163791.	Location/Qualifiers
		1..13652
		Source

FEATURES	SOURCE
Location/Qualifiers	1. .13652
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	/db_xref="taxon:9606"
	/chromosome="17"
	/map="17p13.1"
	1. .2338
intron	/gene="ALOX12B"
	/number=2
	1. .10971
gene	/gene="ALOX12B"
	2339. .2420
exon	/gene="ALOX12B"
	/number=3
	/usedIn=AJ305026:ALOX12B_mRNA
	/usedIn=AJ305026:ALOX12B_CDS
intron	2421. .2549
	/gene="ALOX12B"
	/number=3
	2550. .2642
exon	/gene="ALOX12B"
	/note="exon 4a"
	/usedIn=AJ305026:ALOX12B_mRNA
	/usedIn=AJ305026:ALOX12B_CDS
	2643. .2745
intron	/gene="ALOX12B"
	/note="intron 4a"
	2746. .2868
exon	/gene="ALOX12B"

	intron	/usedIn-AJ305026:AIOX12B_mRNA /usedIn-AJ305026:AIOX12B_CDS 10493..10689 /gene="AIOX12B" /number=13
	exon	10690..10971 /gene="AIOX12B" /number=14
3' UTR	exon	/usedIn-AJ305026:AIOX12B_mRNA /usedIn-AJ305026:AIOX12B_CDS 10868..10971 /gene="AIOX12B" complement(11096..11257) /gene="AIOX15P"
mRNA		/number=14 complement(join(11096..11257,11698..11859,11953..12053, 12129..>12250)) /gene="AIOX15P"
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CDS		complement(join(<11096..11257,11698..11859,11953..12053 12129..>12250)) /gene="AIOX15P"
		/codon_start=1 /pseudo
intron		/product="arachidonate 15-lipoxygenase" complement(11258..11697) /gene="AIOX15P"
exon		/number=13 complement(11698..11859) /gene="AIOX15P"
intron		/number=13 complement(11860..11952) /gene="AIOX15P"
exon		/number=12 complement(11953..12053) /gene="AIOX15P"
intron		/number=12 complement(12054..12128) /gene="AIOX15P"
exon		/number=11 complement(12129..12250) /gene="AIOX15P"
BASE COUNT	3147 a 3653 c 3968 g 2880 t 4 others	
ORIGIN		
Query Match	33.0% Score 121.6; DB 9; Length 13652;	
Best Local Similarity	82.7% Pred. No. 2,7e-20;	
Matches 139; Conservative 0; Mismatches 29; Indels 0; Gaps 0;		
OY 175 TTTCCCTGGGCGCTAGAGGCGTTCGCACAGGTGATGTCGGGGCTCTGTGACTCACCT	234	
Db 7177 TGTCCTGGGCGTGGAAGGCTTTCGTGGGGTGATGGTACGGGCTCTGCGAGCTCACCT	7236	
OY 235 ACAAAAGCCTCGCATTCGCCAACGACTTGTGGAGCGCGGGGTCACGAGCACTGCCTGGGT	294	
Db 7237 ATGACAGCCTCTACTCCCACATGACTTTGTGGACCGTGGGGTCCAGSACCTGCCTGAT	7296	
OY 295 ATTATTTCCTGATGACAGCCTGGCGGCTGTGTACGCGATGAGAGGT	342	
Db 7297 ATTACTACCGGATGACAGCTTGGCGGCTGTGGAAATGCACTGGAGAAT	7244	
RESULT 9		
AC015734	159582 bp DNA linear HTG 13-NOV-2001	
LOCUS	AC015734	
DEFINITION	Homo sapiens clone Rpl1-ID5, WORKING DRAFT SEQUENCE, 13 unordered pieces.	
ACCESSION	AC015734	
VERSION	AC015734.4 GI:16905302	

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http://lcp.genome.washington.edu/RM/RepeatMasker.html
Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WtBR
Web site: http://www.seq.wi.mit.edu
Contact: sequence.submissions@genome.wi.mit.edu
-----
Project Information
Center project name: L1443
Center clone name: L1D_5
-----
Summary Statistics
Sequencing vector: MJ3; M77815; 49% of reads
Sequencing vector: Plasmid; n/a; 51% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 155110 bases at least Q40
Consensus quality: 166980 bases at least Q30
Consensus quality: 157686 bases at least Q20
Insert size: 119000; agarose-fp
Insert size: 158332; sum-of-contigs
Quality coverage: 10.7 in Q20 bases; agarose-fp
Quality coverage: 8.1 in Q20 bas.
NOTE: This is a 'working draft' sequence. It currently
consists of 13 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.
1      1480: contig of 1480 bp in length
1481 1580: gap of 100 bp
1581      2920: contig of 1340 bp in length
2921 3020: gap of 100 bp
3021      6224: contig of 3204 bp in length
6225 6324: contig of 100 bp
6325      13162: contig of 6838 bp in length
13163 13262: gap of 100 bp
13263      19152: contig of 5890 bp in length
19153 19252: gap of 100 bp
19253      73423: contig of 54171 bp in length
73424 73523: gap of 100 bp
73524      81434: contig of 7911 bp in length
81435 81534: gap of 100 bp

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Query Match	32.0%;	Score 121.6;	DB 2;	Length 159582;
Best Local Similarity	82.7%;	Pred. 11.8e-20;		
Matches 139;	Conservative 0;	Mismatches 29;	Indels 0;	Gaps 0
QY 175	TTTCCCTGGGGCCCTAGAGGCGTTTGGCACAGGTGATGTGTCGGGCTGTCTGAGCTCACT	234		
Db 157766	TGTCCCTGGGGCGTGGAGGCTTTGCTGGGGGATGTGTAGCGGCTCTCTGGAGCTCACT	157825		
QY 235	ACAAAGCCCTCTGCATTTCCCAAGCACTTTGTGTGAGACGGGGGCTCCAGAGCACTGGCTGAGGT	294		
Db 157826	ATGCACACCCCTCTCACTCCCAATGAATGTTGTGAGACGGTGGGGTCCAGGACCTGGCTTGAT	157885		
QY 295	ATTATTTCCTGATGAGACAGCGCTGGCGGCTGTGGTAGCGCATGGAGAGGT	342		
Db 157886	ATTACTACCGCGCATGACACAGCTTGGCGCGTGTGSAATGCACACTGGAGAGGT	157933		

RESULT 10

LOCUS MM018477

DEFINITION Mus musculus Alox12b gene 5', flanking region.

ACCSSION Y18477

3626 bp DNA linear ROD 14-APR-1999

VERSION V18477.1 GI:4586204
 KEYWORDS 12(R)-lipoxygenase; Alox12B gene.
 SOURCE mouse mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 3626)
 AUTHORS Krieg, P., Siebert, M., Kinzig, A., Bettenhausen, R., Marks, F. and Furstemberger, G.
 TITLE Murine 12(R)-lipoxygenase: functional expression, genomic structure and chromosomal localization
 JOURNAL FEBS Lett. 446 (1), 142-148 (1999)
 MEDLINE 99198730
 REFERENCE 2 (bases 1 to 3626)
 AUTHORS Krieg, P.
 TITLE Direct Submission
 JOURNAL Submitted (26-NOV-1998) P. Krieg, German Cancer Research Center, Research Program 2, Im Neuenheimer Feld 280, D- 69120 Heidelberg, FRG
 FEATURES
 source Location/Qualifiers
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 /strain="NMRI"
 /db_xref="taxon:10090"
 /chromosome="11"
 /tissue_type="skin epidermis"
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 /note="5' flanking region"
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 Best Local Similarity 99.0%; Pred. No. 2.1e-15;
 Matches 103; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 3 AAGGACGACCTGCTCCGGCTCCAGAGCATTCGCGGAGACGTTCCGCTGACTGC 62
 1 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 3441 AGGGACGACCTGCTCCGGCTCCAGAGCATTCGCGGAGACGTTCCGCTGACTGC 3500
 1 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 63 TCCATCAGTCAGTCGTCATCACTCTTCGCTGCTGCTTCCT 106
 1 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 3501 TCCATCAGTCAGTCGTCATCACTCTTCGCTGCTGCTTCCT 3544
 1 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 RESULT 11
 HSA305021 4293 bp DNA linear PRI 14-MAR-2001
 DEFINITION Homo sapiens partial ALOXE3 gene for arachidonate lipoxygenase 3, exons 5 to 11.
 ACCESSION AJ305021
 KEYWORDS AJ305021.1 GI:13374915
 SOURCE ALOXE3 gene; arachidonate lipoxygenase 3.
 ORGANISM human.
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE 1 (bases 1 to 4293)
 AUTHORS Krieg, P., Marks, F. and Furstemberger, G.
 TITLE A gene cluster encoding human epidermis-type lipoxygenases at chromosome 17p13.1: Cloning, physical mapping, and expression
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 4293)
 AUTHORS Krieg, P.R.
 TITLE Direct Submission
 JOURNAL Submitted (18-AUG-2000) Krieg P.R., Research Program on Tumor Cell Regulation, Deutsches Krebsforschungszentrum, Im Neuenheimer Feld 280, Heidelberg, D-69120, GERMANY
 COMMENT Related sequences: AJ305020 to AJ305031. Overlapping sequence: AC015734.

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 2066..2269
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 2359..2445
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 /number=10
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 Best Local Similarity 58.5%; Pred. No. 0.00035;

Matches	100;	Conservative	0;	Mismatches	71;	Indels	0;	Gaps	0;
QY	177	TCCCTGGCCCTT	MAAGGGCTT	CGCACAGTGATGTT	CGGGGTCGTCTG	AGCTACCTTAC	236		
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QY	237	AAAGCGCTTGAT	TCCCAACGACTT	TGTGAGACGG	GGGGGTCC	AGGACCTGCTGGGTAT	296		
Db	3084	ACCAATTTTCTG	CTTCCGGACAG	CCCTGCGGGCCCG	GGGGCTCTG	GCCTATCCCAACTTAC	3143		
QY	297	TATTTCCCTGAT	GATACAGACCTG	CGGGTGTGTACG	CAATGAGAGGTAC	GTG	347		
Db	3144	CACCTACCGAG	ACAGACGGCCTT	GAAAGATCTCTG	GGCGGGCCATTG	AGAGGTGGCAG	3194		

RESULT	12
AC107913/c	
LOCUS	AC107913
DEFINITION	36006 bp DNA
DESCRIPTION	Human sapiens chromosome 17 clone CTD-3051C7 map 17, LOW-PASS
VERSION	AC107913
KEYWORDS	AC107913.1 GI:18308639
SOURCE	HTG; HTGS_PHASE0.
ORGANISM	human.
	Homo sapiens

REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS

Eukariota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidiinae; Homo.
1 (bases 1 to 36006)
Birtten,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 17, clone CFD-3051C7
Unpublished
2 (bases 1 to 36006)
Birtten,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,

Anderson, S., Barna, N., Bastien, V., Boguslavsky, L., Boukhalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepe, Y., Colangelo, M., Collins, S., Collimore, A., Cook, A., Cooke, P., Derellano, K., Desat, K., Diaz, J. S., Dodge, S., Fato, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gaidyna, S., Glinde, S., Gort, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRoque, K., Lamazares, R., Landers, T., Lehoczy, J., Levine, R., Liu, G., Maclean, C., Macdonald, P., Major, J., Marcum, N., Matthews, C., McCarthy, M., McKean, P., McKernan, K., Meldrum, J., Meneses, L., Milnova, T., Mleniga, V., Murphy, T., Naylor, D., Nguyen, C., Nicol, R., Notdu, C., Notman, C. H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunhkhang, P., Plerre, N., Pollara, V., Raymond, C., Retlau, R., Rieback, M., Riley, R., Risse, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schuppback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, P., Subramanian, A., Talamas, J., Testafaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Triggillo, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. D., Young, G., Zahoun, J., Zembek, L., Zimmer, A. and Zody, M.

TITLE	Direct Submission
JOURNAL	Submitted (24-JAN-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT	All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P (1996-1997)
<http://ftp.genome.washington.edu/M/RepeatMasker.html>
 ----- Genome Center
 Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WIBR
 Web site: <http://www-seq.wi.mit.edu>
 Contact: sequence.submissions@genome.wi.mit.edu
 ----- Project Information
 Center project name: L2304
 Center clone name: 3051_C_7

* NOTE: this record contains 46 individual sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads * and the order in which they appear is completely

* abirrigity Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allow
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.

1	663	762:	gap of	100	bp	in	length
2	763	1441:	contig of	679	bp	in	length
3	1442	1541:	gap of	100	bp	in	length
4	1542	2198:	contig of	657	bp	in	length
5	2199	2296:	gap of	100	bp	in	length
6	2299	2964:	contig of	666	bp	in	length
7	2665	3064:	gap of	100	bp	in	length
8	3065	3711:	contig of	667	bp	in	length
9	3732	3831:	gap of	100	bp	in	length
10	3832	4454:	contig of	703	bp	in	length
11	4535	4634:	gap of	100	bp	in	length
12	4635	5328:	contig of	694	bp	in	length
13	5329	5428:	gap of	100	bp	in	length
14	5429	6124:	contig of	696	bp	in	length
15	6125	6224:	gap of	100	bp	in	length
16	6225	6877:	contig of	653	bp	in	length
17	6878	6977:	gap of	100	bp	in	length
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19	7662	7761:	gap of	100	bp	in	length
20	7762	8436:	contig of	675	bp	in	length
21	8437	8536:	gap of	100	bp	in	length
22	8537	9204:	contig of	668	bp	in	length
23	9205	9304:	gap of	100	bp	in	length
24	9305	9968:	contig of	664	bp	in	length
25	9969	10068:	gap of	100	bp	in	length
26	10069	10766:	contig of	698	bp	in	length
27	10767	10866:	gap of	100	bp	in	length
28	10867	11568:	contig of	702	bp	in	length
29	11569	11668:	gap of	100	bp	in	length
30	11669	12366:	contig of	698	bp	in	length
31	12367	12466:	gap of	100	bp	in	length
32	12467	13130:	contig of	684	bp	in	length
33	13131	13230:	gap of	100	bp	in	length
34	13231	14010:	contig of	760	bp	in	length
35	14011	14110:	gap of	100	bp	in	length
36	14111	14776:	contig of	666	bp	in	length
37	14777	14876:	gap of	100	bp	in	length
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39	15554	15653:	gap of	100	bp	in	length
40	15654	16340:	contig of	687	bp	in	length
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42	16441	17128:	contig of	688	bp	in	length
43	17129	17228:	gap of	100	bp	in	length
44	17229	17929:	contig of	701	bp	in	length
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48	18815	19492:	contig of	678	bp	in	length
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51	20278	20377:	gap of	100	bp	in	length
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57	22602	22701:	gap of	100	bp	in	length
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59	23378	23477:	gap of	100	bp	in	length
60	23478	24112:	contig of	695	bp	in	length
61	24173	24272:	gap of	100	bp	in	length
62	24273	24927:	contig of	655	bp	in	length
63	24928	25027:	gap of	100	bp	in	length
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* 25910 26607: contig of 698 bp in length
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* 27377 27476: gap of 100 bp in length
* 27477 28185: contig of 709 bp in length
* 28186 28285: gap of 100 bp in length
* 28286 28932: contig of 647 bp in length
* 28933 29032: gap of 100 bp in length
* 29033 29272: contig of 695 bp in length
* 29728 29827: gap of 100 bp in length
* 29828 30479: contig of 652 bp in length
* 30480 30579: gap of 100 bp in length
* 31287 31286: contig of 707 bp in length
* 31287 31386: gap of 100 bp in length
* 31387 32075: contig of 689 bp in length
* 32076 32175: gap of 100 bp in length
* 32176 32864: contig of 689 bp in length
* 32865 32964: gap of 100 bp in length
* 32965 33669: contig of 705 bp in length
* 33670 33769: gap of 100 bp in length
* 33770 34458: contig of 689 bp in length
* 34459 34558: gap of 100 bp in length
* 34559 35212: contig of 654 bp in length
* 35213 35312: gap of 100 bp in length
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1. 36006
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BASE COUNT 7672 a 8083 c 7883 g 7763 t 4605 others
ORIGIN

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Query Match 15.1%; Score 57.4; DB 2; Length 36006;
Best Local Similarity 58.5%; Pred. No. 0.00025;
Matches 100; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

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Oy 177 TCCTGGGCGCTAGAGGCTTGGCAGAGTGATGGTGGGCTGTGTGACCTCCTAC 236
Db 34071 TCCATCGGGAGGAGGAGGCTTACCTCTATCTAGCAGAGGCGGCTCCACTCCTAC 34012
Oy 237 AAAAGCCCTCATCTCCAGACTTGTGGAGCGGCGGCTCCAGACTCGGCTAT 296
Db 34011 ACCATTTCTCTCCGAGAGCTTGGGCGGCGGCTCTGCTATCCCACTAC 33952
Db 297 TATTTCCGTATGACAGCGCTGCGGTGATACCGCATGAGAGTACGTG 347
Db 33951 CACTACCGAGAGGAGGCTTGAAGATCTGGGCGGCGCATGTAGAGTGCAG 33901

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RESULT 13
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LOCUS Homo sapiens clone RP11-1D5, WORKING DRAFT SEQUENCE, 13 unordered
DEFINITION pieces.
ACCESSION AC015734
VERSION AC015734.4 GI:16905302
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 159582)
AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.
TITLE Homo sapiens, clone RP11-1D5
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 159582)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
Baldwin,J., Batra,N., Beckerly,R., Boguslavsky,L., Boukhgalter,B.,

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TITLE JOURNAL COMMENT

Brown,A., Castle,A., Colangelo,M., Collins,S., Collimore,A.,
Cooke,P., Dearellano,K., Dewar,K., Domino,M., Donelan,L., Doyle,M.,
Ferreira,P., Fitzhugh,W., Forrest,C., Funke,R., Gage,D.,
Galagan,J., Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L.,
Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,
Lehoczky,J., Lieu,C., Locke,K., Macdonald,P., Marquis,N.,
McEwan,P., McGurk,A., McKernan,K., McLaughlin,J., Melidim,J.,
Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
Peterson,K., Pollara,V., Riley,R., Roy,A., Santos,R., Severy,P.,
Strange-Thomann,N., Stojanovic,N., Sudranalan,A., Talamas,J.,
Testaye,S., Tlrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X.,
Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.

Submitted (17-NOV-1999) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Nov 13, 2001 this sequence version replaced g1.7543748.
All repeats were identified using RepeatMasker:
Smit,A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: <http://www.seq.wi.mit.edu>
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: 1J433
Center clone name: 1J.D-5

----- Summary Statistics
Sequencing vector: M13; W77815; 49% of reads
Sequencing vector: Plasmid; n/a; 51% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 155110 bases at least Q40
Consensus quality: 157688 bases at least Q20
Insert size: 115000; agarose-rp
Insert size: 158382; sum-of-contigs
Quality coverage: 10.7 in Q20 bases; agarose-rp
Quality coverage: 8.1 in Q20 bas.

NOTE: This is a 'working draft' sequence. It currently
consists of 13 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.

```

* 1 1480: contig of 1480 bp in length
* 1481 1580: gap of 100 bp in length
* 1581 2920: contig of 1340 bp in length
* 2921 3020: gap of 100 bp in length
* 3021 6224: contig of 3204 bp in length
* 6225 6324: gap of 100 bp in length
* 6325 13162: contig of 6838 bp in length
* 13163 13262: gap of 100 bp in length
* 13263 19152: contig of 5890 bp in length
* 19153 19252: gap of 100 bp in length
* 19253 73423: contig of 54171 bp in length
* 73424 73523: gap of 100 bp in length
* 73524 81434: contig of 7911 bp in length
* 81435 81534: gap of 100 bp in length
* 81535 91266: contig of 9732 bp in length
* 91267 91366: gap of 100 bp in length
* 91367 104881: contig of 13515 bp in length
* 104882 104981: gap of 100 bp in length
* 104982 117370: contig of 12389 bp in length
* 117371 117470: gap of 100 bp in length
* 117471 133737: contig of 16267 bp in length
* 133738 133837: gap of 100 bp in length
* 133838 155551: contig of 21714 bp in length
* 155552 155651: gap of 100 bp in length
* 155652 159582: contig of 3931 bp in length.
Location/Qualifiers

```

FEATURES

Query Match	15.1%	Score 57.4	DB 2	Length 159562
Best Local Similarity	58.5%	Pred. No. 0.00019		
Matches 100	Conservative 0	Mismatches 71	Indels 0	Gaps 0
Oy 177	TCCTGGGCGCTGAGGCGCTTCCGACAGTGTAGTGGTGGGGTGTGTGAGCTACCTAC	236		
Db 50049	TCGATGGGAGGCGAAGCGCCCTCATCTACCTATGAGACAGGGCCCTGGCCCTCACCCTAC	49930		
237	AAAAGCCTCGCATTCGCCAACGACTTTTGTGAGGCGGGGCGCCAGGACCTCGCTGGGTAT	296		
Db 49989	ACCAATTTCTGCCTTCCGAGACAGCTGGGGGCCCGCGGCTCTGGGTATCCCAACTAC	49930		
Oy 297	TATTTCCGCGATGACACAGCTGGCGGTGTGTGTACCGCATGTGAGAGTACGTG	347		
Db 49929	CACCTACGAGACAGCGCGCTGAAAGATCTGGCGGCCCATTTGAGAGGTGCGAG	49879		
RESULT 14				
AX304470				
LOCUS	AX304470	2136 bp	DNA	
DEFINITION	Sequence 8 from Patent WO0185956.			
ACCESSION	AX304470			
VERSION	AX304470.1	GI:17383841		
KEYWORDS	human.			
SOURCE	human.			
ORGANISM	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
REFERENCE	1 (sites)			
AUTHORS	Das, D., Reddy, R., Yao, M. G., Nguyen, D. B., Lu, Y., Tibboulcy, C. M.,			
	Yue, H., Khan, F. A., Gandhi, A. R., Au-Yang, J., Lai, P., Kearney, L.,			
	Elliott, V. S., Ding, L. and Thornton, M.			
	Lipid metabolism enzymes			
TITLE	Patent: WO 0185956-A 8 15-NOV-2001;			
JOURNAL				

RESULT	15
LOCUS	AF182218
DEFINITION	AF182218 Homo sapiens epidermal lipoxigenase (ALOXE5) mRNA, linear PRI 01-OCT-2000
ACCESSION	AF182218
VERSION	AF182218.1 GI:10441003
KEYWORDS	.
SOURCE	human.
ORGANISM	Homo sapiens Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 3082) Brash,A.R. and Boeglin,W.E. Human epidermal lipoxigenase, ortholog of mouse Aloxex3 Unpublished 2 (bases 1 to 3082) Brash,A.R. and Boeglin,W.E. Direct Submission Submitted (01-sep-1999) Clinical Pharmacology, Vanderbilt University, MRI 510 23rd Ave S. at Pierce, Nashville, TN 37232-6602, USA Location/Oualifiers I..3082
FEATURES	
Source	

FEATURES	
source	Location/Qualifiers
gene	1..3082 /organism="Homo sapiens" /db_xref="taxon:9606" 1..3082
CDS	/gene="ALOXE3" 202..2337 /gene="ALOXE3" /note="similar to mouse ALOXE3" /codon_start=1 /product="epidermal 11oxygenase" /protein_id="AAG16899.1" /db_xref="GI:10441004" /translation="MAVRYLCVTTGPLYLRAGTLNDINISVLTGTCGSESPKRLDIRMGDRFAPSPVQRYKRCFAELGELLRLVRKEVAFRRDSWYCSITVTEBDSGVSPHPQOMIGQYVELRGVGTARTICODSLPLIDRLPRLAROEYRKITVAPGSGNPDVNTSFQMEDSKKFALETKITTCVGDGSSGNTYGLGEMKIDIPSLAMPEPNVYVSTKITSLFNALPAGISGMKIRGLIDRSGSKKLDMDONTMFCWKHPTTKYVTEHNCEDDFPEGYLNCVAVPMILHICISLPSKLYPTNDMAVPLIGDOTCLQTEHERENITFLAYWLLAEPYTHLNRQOYVAPLCLWLSPGALVELATLQISOTGPPSPILFPLTDEFWMLLKTWVNSSEFLHENNTHFLCTHLLCEAFAMATLRDLCPHPIYKLLPHTRTVTLQVNT

BASE COUNT	ORIGIN
676 a	996 c 769 g 641 t
ARALLNPEGIVDOVTSIGRGLIYLASTGASHHTYANFCLIPSDLRARGVLAIPNHY RDDELKLTWAAIEGVSEVSEIYGYPSDVOODSELTQATGIEFAQALIGRESSGFPSS CLTPGEWVKPLTTLAIIFENCSAOHAAVNSGDHGFMMNAPMSMOPPORRGTTLLTKK YLIDPLREVNTSCNNLLIPMLYSOERKDPORRGITPDDEHFTTEARSRSLAAQSLAQI SRDLOENOGCLAPYTYLIDPLLENYSYI"	

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: May 24, 2002, 18:05:53 ; Search time 1935.21 Seconds
(without alignments)
2650.277 Million cell updates/sec

Title: W36511
Perfect score: 380
Sequence: 1 GCAAGCAGCAGCTCTCC.....ACTTATTATTCACCAATGAC 380

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 segs, 6748477542 residues
Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
EST:
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrtl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	380	100.0	380	10 W36511	W36511 mb76f09.r1
2	185.2	48.7	462	10 AA760573	AA760573 vv78h03.r
3	174.8	46.0	361	10 W10508	W10508 ma40f06.r1
4	151.4	39.8	553	10 BF466248	BF466248 UT-M-CGDP
5	131.6	34.6	645	10 BG436629	BG436629 602489125
6	121.6	32.0	425	10 BG946103	BG946103 MR3-KT005
7	115	30.3	499	9 AM488090	AM488090 UI-M-BH3-
8	114.6	30.2	818	10 BG698713	BG698713 602703088
9	100.4	26.4	795	10 B1667266	B1667266 603292520
10	97	25.5	100	10 W18678	W18678 mb98f01.r1
11	93.4	24.6	518	9 A1788059	A1788059 u116g08.y
12	89.8	23.6	214	10 W11802	W11802 mb22h02.r1
13	88	23.2	214	9 BB587762	BB587762 BB587762
14	80.4	21.2	257	9 AA038641	AA038641 m194a06.r
15	80.4	21.2	449	9 A1385442	A1385442 m194a06.y
16	75	17.7	277	10 BE715737	BE715737 CM4-HT05
17	66.4	17.5	445	10 BF464406	BF464406 UT-M-CGDP

C	18	55.4	14.6	433	9	AM047244	UT-M-BH1-
	19	52.6	13.8	479	9	A0243940	A0243940 A0243940
	20	50	13.2	605	10	B1489877	B1489877 603031627
	21	50	13.2	761	10	BG740246	BG740246 602630664
	22	50	13.2	833	10	BG675395	BG675395 602621712
	23	50	13.2	840	10	BG740579	BG740579 602633094
	24	50	13.2	845	10	BG740763	BG740763 602632735
	25	50	13.2	876	10	BG674800	BG674800 602620931
	26	50	13.2	892	10	BG743633	BG743633 602633993
	27	50	13.2	893	10	BG741964	BG741964 602633405
	28	49.4	13.0	628	9	BB378807	BB378807 BB378807
	29	49.4	13.0	669	12	AG090131	AG090131 Pen trogl
	30	48.8	12.8	843	10	BG739709	BG739709 602630403
	31	48.8	12.8	863	10	BG696031	BG696031 602658180
	32	48.4	12.7	556	12	BH088160	BH088160 RPCI-24-3
	33	47.4	12.5	361	9	A1324883	A1324883 m194a06.x
	34	45	11.8	865	10	BG742611	BG742611 602633205
	35	43.6	11.5	550	12	A0594148	A0594148 HS-5334-A
	36	40.6	10.7	350	9	AM158910	AM158910 z49a08.x
	37	40	10.5	813	10	BF674881	BF674881 602136749
	38	38.4	10.1	832	10	BG698185	BG698185 602660087
	39	37.8	9.9	765	10	BG934596	BG934596 SK1-0908
	40	36.5	9.6	415	10	BE483723	BE483723 170000 BA
	41	36.4	9.6	841	10	BG483904	BG483904 602504481
	42	35.6	9.4	446	9	BB732451	BB732451 BB732451
	43	35.4	9.3	414	10	BE982417	BE982417 UT-M-CGDP
	44	35.4	9.3	697	10	BG739860	BG739860 602630592
	45	35.2	9.3	429	9	AV608986	AV608986 AV608986

ALIGNMENTS

RESULT 1
W36511 380 bp mRNA linear EST 11-SEP-1996
LOCUS mb76f09.r1 Soares mouse p3NMf19.5 Mus musculus cDNA clone
DEFINITION IMAGE:335369 5' similar to SW:10X2_HUMAN P18054 ARACHIDONATE
12-LIPOXYGENASE, c. mRNA sequence.
W36511
VERSION W36511.1 GI:1318416
KEYWORDS house mouse.
SOURCE Mus musculus.
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE 1 (bases 1 to 380)
Marras,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,D., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
The WashU-HMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Email: mouseest@wustl.wustl.edu
This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:216769

TITLE The WashU-HMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT WashU-HMI Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Email: mouseest@wustl.wustl.edu
This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:216769
Possible reversed clone: similarly on wrong strand
Seq primer: ETPRimer
High quality sequence stop: 332.
Location/Qualifiers
1. 380
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:335369"
/clone_lib="Soares mouse p3NMf19.5"

FEATURES

source

JOURNAL Unpublished (1996)
COMMENT Contact: Maria M/Mouse EST Project
WashU-HMHT Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu
This clone is available royalty-free through LBNL; contact the
IMAGE Consortium (info@image.lbnl.gov) for further information.
MGI: 203803
Seq primer: mod.REGA+ET
High quality sequence stop: 337.
Location/Qualifiers
1. 361
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/db_xref="taxon:10090"
/clone_lib="Soares mouse p3NMF19.5"
/dev_stage="19.5 dpc total fetus"
/lab_host="DH10B (ampicillin resistant)"
/note="Vector: pT7R3D (Pharmacia) with a modified
polylinker. Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAGAGTGGAGCGGCGCATTTTCTTTTCTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT7R3 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by Bento
Soares and M. Fatima Bonaldo. RNA was kindly provided by
Dr. Minoru Ko (Wayne State University)."

BASE COUNT 79 a 92 c 108 g 82 t
ORIGIN

Query Match 46.0%; Score 174.8; DB 10; Length 361;
Best Local Similarity 98.0%; Pred. No. 8.9e-41;
Matches 198; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

175 TTTCCTGGGCTAGAGGCTTGCACAGGTGATGGTGGGCTGCTGAGCTACCT 234
7 TGTCCTGGGCTAGAGGCTTGCACAGGTGATGGTGGGCTGCTGAGCTACCT 65
235 ACAAAAGCCTCTGCATTCGCCAGAGCTTGTGAGAGCGGGGTCAGAGACTGCTGGT 294
66 ACAAAAGCCTCTGCATTCGCCAGAGCTTGTGAGAGCGGGGTCAGAGACTGCTGGT 125
295 ATTATTTCCGTGATGACAGCTGCGGTGTGATGCGGATGAGAGCTGCTGAGAG 354
126 ATTATTTCCGTGATGACAGCTGCGGTGTGATGCGGATGAGAGCTGCTGAGAG 184
355 ATCATCACTATTATTACCAAA 376
185 ATCATCACTATTATTACCAAA 206

RESULT 4
BF466248 553 bp mRNA linear EST 04-DEC-2000
LOCUS BF466248
DEFINITION UI-M-CG0p-bqv-c-02-0-UI.s1 NIH_BMAP_Ret4_S2 Mus musculus cDNA clone
VERSION UI-M-CG0p-bqv-c-02-0-UI 3', mRNA sequence.
ACCESSION BF466248.1 GI:11535431
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 553)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
discovery

JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
COMMENT Contact: Chin, H
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
20892-9643, USA
Tel: 301 443 1706
Fax: 301 443 9890
Email: MEST@mail.nih.gov
Oligo-dT track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.B.
Soares Lab Clone Distribution: Researchers may obtain BMAP cDNA
clones from RESEARCH GENERICS. It should be noted that Bento Soares
is generating a small number of additional specialized
non-redundant arrays of BMAP cDNAs whose availability will be
considered under appropriate and limited collaborative arrangements
Seq primer: M13 Forward
PolyA-No.

FEATURES
source location/Qualifiers
1. 553
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone_lib="UI-M-CG0p-bqv-c-02-0-UI"
/clone_lib="NIH_BMAP_Ret4_S2"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT7R3D-Pac (Pharmacia) with a modified
polylinker. Site 1: Not I; Site 2: Eco RI; The
NIH_BMAP_Ret4_S2 library is a subtracted library,
ultimately derived from mouse retina tissue libraries at
various stages of development. For a detailed description
of the library from which this clone was derived, please
visit our web site at brainest.eng.uiowa.edu.
TAG_SEQ=None found"

BASE COUNT 121 a 156 c 152 g 123 t 1 others
ORIGIN

Query Match 39.8%; Score 151.4; DB 10; Length 553;
Best Local Similarity 97.9%; Pred. No. 8.1e-34;
Matches 185; Conservative 0; Mismatches 1; Indels 3; Gaps 3;

188 AAGAGGCTTGCACAGGTGATGGTGGGCTGCTGAGCTACCTACAAAGCCTCTG 247
553 AAGAGGCTTGCACAGGTGATGGTGGGCTGCTGAGCTACCTACAAAGCCTCTG 495
248 CATTCCCAAGCACTTGTGAGAGCGGGGTCAGAGACTGCTGGTATTATTCCGCGA 307
494 CATTCCCAAGCACTTGTGAGAGCGGGGTCAGAGACTGCTGGTATTATTCCGCGA 436
308 TGACAGCCTGCGGCTGTGATGCGGATGAGAGTACCTGATCATCACTATT 367
435 TGACAGCCTGCGGCTGTGATGCGGATGAGAGTACCTGATCATCACTATT 377

368 ATTACCAAA 376
376 ATTACCAAA 368
RESULT 5
BG436629 645 bp mRNA linear EST 14-MAR-2001
LOCUS BG436629
DEFINITION 602489125P1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4620966 5',
mRNA sequence.
ACCESSION BG436629
VERSION BG436629.1 GI:13343135
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 645)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.

20892-9643, USA
 Tel: 301 443 1706
 Fax: 301 443 9890
 Email: mestr@mail.nih.gov
 Oligo-dT track not found. Not I site shown in beginning of sequence is likely internal to the message. cDNA Library Preparation: M.B. Soares Lab Clone Distribution: Researchers may obtain BMAP cDNA clones from RESEARCH GENETICS. It should be noted that Benito Soares is generating a small number of additional specialized non-redundant arrays of BMAP cDNAs whose availability will be considered under appropriate and limited collaborative arrangements
 Seg primer: M13 Forward
 POLY-A-

FEATURES

Source Location/Qualifiers
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 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UT-M-BH3-art-e-11-0-UT"
 /clone_lib="NIH-BMAP-M_S4"
 /dev_stage="27-32 days"
 /lab_host="DH10B (Life Technologies)"
 /note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker. Site 1: Not I; Site 2: Eco RI; The NIH-BMAP-M_S4 library is a subtracted library of a series, ultimately derived from a mixture of individually tagged normalized libraries from ten regions of the mouse brain (cerebellum, brain stems, olfactory bulbs, hypothalamus, cortex, amygdala, basal ganglia, pineal gland, striatum, hippocampus) after a series of subtractions to reduce the representation of cDNAs from which ESTs had already been generated. The following serially subtracted libraries were generated in this process: NIH-BMAP-M_S3.1, NIH-BMAP-M_S3.3, NIH-BMAP-M_S3.2, NIH-BMAP-M_S3.1, NIH-BMAP-M_S2, NIH-BMAP-M_S1. The subtracted library (NIH-BMAP-M_S4) was constructed as follows: PCR amplified cDNA inserts from NIH-BMAP-M_S3.3, NIH-BMAP-M_S3.2, and NIH-BMAP-M_S3.1 clones from which 3' ESTs had been derived was used as a driver in a hybridization with a pool of the NIH-BMAP-M_S3.3, NIH-BMAP-M_S3.2, and NIH-BMAP-M_S3.1 libraries in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DH10B bacteria (Life Technologies) to generate the NIH-BMAP-M_S4 library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1996)
 TAG-lib=NIH-BMAP-M_S4
 TAG-TISSUE=basal-ganglia
 TAG-SEQ=TGAC
 BASE COUNT 107 a 139 c 142 g 111 t
 ORIGIN

Query Match 30.3%; Score 115; DB 9; Length 499;
 Best Local Similarity 95.6%; Pred. No. 3.8e-23;
 Matches 129; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

242 CCTGTGATTCACAGAGCTTTGTGAGCGCGGGGTCAGAGCTGCTGGTATTATT 301
 |||||||
 Db 499 CCTGTGATTCACAGAGCTTTGTGAGCGCGGGGTCAGAGCTGCTGGTATTATT 440
 |||||||
 302 CCGTGATGACAGCGCTGGGTGTGAGCGAGAGAGTACTGACTAGACATCATCA 361
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 Db 439 CCGTGATGACAGCGCTGGGTGTGAGCGAGAGAGTACTGACTAGACATCATCA 381
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 362 CTATATTATACCAA 376
 |||||||
 Db 380 CTATATTATACCAA 366

RESULT 8

B6698713 818 bp mRNA linear EST 07-MAY-2001
 LOCUS 602703086F1 NCL_CGAP_Skn3 Homo sapiens cDNA clone IMAGE:4800620 5',
 DEFINITION mRNA sequence.
 ACCESSION B6698713
 VERSION B6698713.1 GI:13966275
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 818)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs@mail.nih.gov
 Tissue Procurement: James Cleaver, M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LHAM10691 row: 0 column: 21
 High quality sequence stop: 779.

FEATURES

Source Location/Qualifiers
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 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:4800620"
 /clone_lib="NCL_CGAP_Skn3"
 /lab_host="DH10B (TI phage-resistant)"
 /note="Organ: skin; Vector: pCMV-Sport6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.5kb. Library constructed by Life Technologies. Note: this is a NCL_CGAP Library."
 BASE COUNT 158 a 250 c 237 g 173 t
 ORIGIN

Query Match 30.2%; Score 114.6; DB 10; Length 818;
 Best Local Similarity 75.6%; Pred. No. 6.3e-23;
 Matches 155; Conservative 0; Mismatches 49; Indels 1; Gaps 1;

175 TTTCCTGGGCGCTAGAGGGGTTGGACAGTATGTTGGGCTGTGTGACCTACT 234
 |||||||
 Db 417 TGTCCCTGGGCGGTGAAGGCTTGTGGGTGATGATGAGGCTGTGAGCTACCT 476
 |||||||
 235 ACAAAAGCCTTGCAATTCACAG-ACCTTTGTGAGCGCGGGGTCAGAGCTGCTGGG 293
 |||||||
 Db 477 ATGACAGCCTCTACCTCCCAATGACCTTTGTGAGCGGTGGGTCAGAGCTGCTGGA 536
 |||||||
 294 TATTATTCCGTGATGACAGCTGGGCTGTGATCGGATGAGAGTACTGACTAGA 533
 |||||||
 Db 537 TATTACTACCGCATACAGCTTGGGATGTGGAATGACGTGAGAAATATATGACGGA 596
 |||||||
 354 GATCATCACTTATTATTACCAATG 378
 |||||||
 Db 597 GATCATCACTTATTATTACCGCAAG 621

RESULT 9
 B1667266 795 bp mRNA linear EST 12-SEP-2001
 LOCUS 603292520P1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:5311901 5',
 DEFINITION mRNA sequence.
 ACCESSION B1667266
 VERSION B1667266.1 GI:15581499
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 795)
 AUTHORS NIH-MGC <http://mhc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Miklos Palokovits, M.D., Ph.D.
 CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
 Toshiyuki and Piero Carninci (RIKEN)
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNLN at:
<http://image.llnl.gov>
 Plate: LLM11790 row: 9 column: 06
 High quality sequence stop: 740.

FEATURES
 source
 1..795
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:5311901"
 /clone_lib="NIH MGC_96"
 /tissue_type="hypothalamus"
 /lab_host="DH10B"
 /note="Organ: Brain; Vector: pBluescript (modified
 pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcagag
); Oligo-dt primed using primer 5'-TTTTTTTTTTTIVN-3',
 size-selected for average insert size 2.3 kb and
 normalized to 10^5. This is a primary library enriched
 for full-length clones and constructed using the
 Cap-trapper method (Carninci, in preparation). Library
 constructed by M. Brownstein (NHGRI/NHGRI, National
 Institutes of Health). Note: this is a NIH-MGC Library."

BASE COUNT 153 a 256 c 228 g 158 t
 ORIGIN

Query Match 26.4%; Score 100.4; DB 10; Length 795;
 Best Local Similarity 82.5%; Pred. No. 9.3e-19;
 Matches 127; Conservative 0; Mismatches 26; Indels 1; Gaps 1;

QY 175 TTTCCCTGGGCTAGAGGGCTTCGACAGGTGATGGTGGGGCTGTGTGACCTCCT 234
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 DB 597 TGTCCCTGGGCTAGAGGGCTTCGACAGGTGATGGTGGGGCTGTGTGACCTCCT 656
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 QY 235 ACAAAAGCCTTCGATTCACAGACGCTTGTGAGGCGGCGGCTCCAGACCTGCGGT 294
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 DB 657 ATGACACGCTCTAC-TCGCCAATGACTTGTGTGAGGCGGCGGCTCCAGACCTGCGGT 715
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 QY 295 ATTATTCGCTGATGACAGCTTCGCGGTGTGTA 328
 ||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 DB 716 TTTTACTACCGCATGACAGCTTCGCGGTGTGTA 749

RESULT 10
 W18678 100 bp mRNA linear EST 12-SEP-1996
 LOCUS mb98601.r1 Soares mouse p3NM19.5 Mus musculus CDNA clone
 DEFINITION IMAGE:337465.5 similar to SW:IOX5_RAT P12527 ARACHIDONATE
 5-LIPOXYGENASE; mRNA sequence.
 ACCESSION W18678
 VERSION W18678.1 GI:1538238
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 100)
 AUTHORS Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
 Geisler, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
 Schellenberg, K., Steptoe, M., Tan, F., Underwood, R., Moore, B.,
 Theising, B., Wylie, T., Lennon, C., Soares, B., Wilson, R. and

TITLE The WashU-HMI Mouse EST project
 JOURNAL Unpublished (1996)
 COMMENT On Sep 12, 1996 this sequence version replaced gi:1294386.
 Contact: Marra M/Mouse EST Project
 WashU-HMI Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810

Trace considered overall poor quality
 This clone is available royalty-free through LNLN; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:218865
 Possible reversed clone: similarity on wrong strand
 Seq primer: -28M13 rev2 from Amerisham
 High quality sequence stop: 1.
 location/Qualifiers
 1..100
 /organism="Mus musculus"
 /db_xref="taxon:10090"
 /clone="IMAGE:337465"
 /clone_lib="Soares mouse p3NM19.5"
 /dev_stage="19.5 ope total fetus"
 /lab_host="DH10B (ampicillin resistant)"
 /note="Vector: pT73D (Pharmacia) with a modified
 polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
 was primed with a Not I - oligo(dT) primer 15',
 TGTTCACATCTGACATGCGAGCGGCGGATTTTCTTTTCTTTT 3',
 double-stranded cDNA was size selected, ligated to Eco RI
 adapters (Pharmacia), digested with Not I and cloned into
 the Not I and Eco RI sites of a modified pT73 vector
 (Pharmacia). Library went through one round of
 normalization to a Cot = 5. Library constructed by Bento
 Soares and M. Fatima Bonaldo. RNA was kindly provided by
 Dr. Minoru Ko (Wayne State University)."

BASE COUNT 19 a 28 c 31 g 22 t
 ORIGIN

Query Match 25.5%; Score 97; DB 10; Length 100;
 Best Local Similarity 100.0%; Pred. No. 3.6e-18;
 Matches 97; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 188 AGAGGCTTCGACAGGTGATGCTTGGGCTGTGTGAGCTCACCAAAAGCCTCTG 247
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 DB 4 AGAGGCTTCGACAGGTGATGCTTGGGCTGTGTGAGCTCACCAAAAGCCTCTG 63
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 QY 248 CATTCACACGACTTGTGAGGCGGCGGCTCCAGAC 284
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 DB 64 CATTCACACGACTTGTGAGGCGGCGGCTCCAGAC 100

RESULT 11
 A1788059 518 bp mRNA linear EST 02-JUL-1999
 LOCUS u116908.y1 Sugano mouse embryo mewa Mus musculus CDNA clone
 DEFINITION IMAGE:208774.5 similar to IR:070582 070582 ARACHIDONATE
 12-LIPOXYGENASE, PSEUDOGENE 2; mRNA sequence.
 ACCESSION A1788059
 VERSION A1788059.1 GI:5335775
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 518)
 AUTHORS Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,
 Underwood, R., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person
 B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Riller
 E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,
 Waterston, R. and Wilson, R.

TITLE The WashU-NCI Mouse EST Project 1999
JOURNAL Unpublished (1999)
COMMENT Contact: Marra M/MashU-NCI Mouse EST Project 1999
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@wustl.edu
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (infoimage.llnl.gov) for further information.
 MGI:995458
 Seq primer: custom primer used
 High quality sequence stop: 518.
FEATURES
 source
 1..518
 /organism="Mus musculus"
 /strain="C57BL"
 /db_xref="taxon:10090"
 /clone="IMAGE:2087774"
 /clone_lib="Sugano mouse embryo mewa"
 /dev_stage="embryo, 14 dpc"
 /lab_host="DH10B"
 /note="Vector: pME18S-FL3; Site 1: DraIII (CACTGCTG);
 Site 2: DraIII (CACCAGTGG); 1st strand cDNA was primed
 with an oligo(dT) primer [ATGTGGCTTTTCTTTTCTTTT];
 double-stranded cDNA was ligated to a DraIII adaptor
 [CTGTGGCTCTAGTGG], digested and cloned into distinct DraIII
 sites of the pME18S-FL3 vector (5' site CACTGCTG, 3' site
 CACCAGTGG). XhoI should be used to isolate the cDNA
 insert. Size selection was performed to exclude fragments
 <1.5kb. Library constructed by Dr. Sumio Sugano
 (University of Tokyo Institute of Medical Science).
 Custom primers for sequencing: 5' end primer
 CTTCCTCTCTAAAGCTGCG and 3' end primer
 CGACCTGCACGCTGACACA."

BASE COUNT 98 a 151 c 142 g 127 t
ORIGIN

Query Match 24.6%; Score 93.4; DB 9; Length 518;
 Best Local Similarity 98.9%; Pred. No. 8.7e-17;
 Matches 94; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 GCTGCTCCGCGTCAGAGCATTCGGGGACAGTGTCCCGCTGACCTCATCACT 71
 |||||||
Db 1 GCTGCTCCGCGCTCCAGAGCATTCGGGGACAGTGTCCCGCTGACCTCATCACT 60
 |||||||
 72 GACTGCTCATCACTCTTCGCTGCTGCTTCCT 106
 |||||||
Db 61 GACTGCTCATCACTCTTCGCTGCTGCTTCCT 95
 |||||||

RESULT 12
W1802 214 bp mRNA linear EST 02-OCT-1997
LOCUS mb22202.r1 Soares mouse p3NNP19.5 Mus musculus cDNA clone
DEFINITION IMAGE:330195.5 similar to P3NNP19.5_RAT P12527 ARACHIDONATE
 5-LIPOXYGENASE; mRNA sequence.
ACCESSION W1802
VERSION W1802.1 GI:1286106
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 214)
AUTHORS Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
 Geisler, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
 Scheinberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
 Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
 Waterston, R.
TITLE The WashU-HM Mouse EST Project
JOURNAL Unpublished (1996)

COMMENT Contact: Marra M/Mouse EST Project
 WashU-HM Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@wustl.edu
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (infoimage.llnl.gov) for further information.
 MGI: 211595
 Possible reversed clone: similarity on wrong strand
 Seq primer: mob.REGA+ET
 High quality sequence stop: 177.
FEATURES
 source
 1..214
 /organism="Mus musculus"
 /db_xref="taxon:10090"
 /clone="IMAGE:330195"
 /clone_lib="Soares mouse p3NNP19.5"
 /dev_stage="19.5 dpc total fetus"
 /lab_host="DH10B (ampicillin resistant)"
 /note="Vector: pRT3D (Pharmacia) with a modified
 polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
 was primed with a Not I - oligo(dT) primer [5'
 TCTTACCAATCTGACAGTGGAGGCGCCGATTCTTTTCTTTT 3']
 double-stranded cDNA was size selected, ligated to Eco RI
 adaptors (Pharmacia), digested with Not I and cloned into
 the Not I and Eco RI sites of a modified pRT3 vector
 (Pharmacia). Library went through one round of
 normalization to a Cot = 5. Library constructed by Benito
 Soares and M. Fatima Bonaldo. RNA was kindly provided by
 Dr. Minoru Ko (Wayne State University)."

BASE COUNT 46 a 53 c 68 g 47 t
ORIGIN

Query Match 23.6%; Score 89.8; DB 10; Length 214;
 Best Local Similarity 97.1%; Pred. No. 6.7e-16;
 Matches 102; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 272 CGGGGTCAGAGCTGCTGCTGATTTATTTCCGTATGACAGCTGGCGTGTACGC 331
 |||||||
Db 1 CGGGGTCAGAGCTGCTGCTGATTTATTTCCGTATGACAGCTGGCGTGTACGC 60
 |||||||
QY 332 GATGAGAGGTAGCTGATCATCATCATATATATACCAA 376
 |||||||
Db 61 GATGAGAGGTAGCTGATCATCATCATATATATACCAA 104
 |||||||

RESULT 13
BB587762 214 bp mRNA linear EST 30-NOV-2000
LOCUS BB587762 RIKEN full-length enriched, adult female vagina Mus
DEFINITION musculus cDNA clone 9930104L01.5, mRNA sequence.
ACCESSION BB587762
VERSION BB587762.1 GI:11484306
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 214)
AUTHORS Aizawa, K., Akahira, S., Akimura, T., Arai, A., Arakawa, T., Carninci, P.,
 Hanagaki, T., Hayatsu, N., Hirooka, T., Hirozane, T., Hodooyama, Y.,
 Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kawai, J., Kojima, Y., Kono
 H., Kusakabe, M., Matsuyama, T., Miyazaki, A., Nakamura, M., Nishii, K.,
 Nomura, K., Numazaki, R., Okazaki, Y., Okido, T., Owa, C., Sakai, C.,
 Sakai, K., Sasaki, D., Sato, K., Shibata, R., Shibata, Y., Shinagawa, A.,
 Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takehashi, F., Tanaka
 T., Toya, T., Watabiki, A., Yamamura, T., Yasunishi, A., Yoshida, K.,
 Yoshiki, A., Muramatsu, M. and Hayashizaki, Y.
TITLE RIKEN Mouse ESTs (Aizawa, K. et al. 2000)
JOURNAL Unpublished (2000)

COMMENT

Contact: Yoshinide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/

Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S., Sasaki, N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Thermotabilization and thermoeactivation of thermostable enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh, M., Katsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.
Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
Please visit our web site (http://genome.rtc.riken.go.jp) for further details.

FEATURES

SOURCE

1. .214
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="930104L01"
/clone_11b="RIKEN full-length enriched, adult female vagina"
/sex="female"
/tissue_type="vagina"
/dev_stage="adult"
/lab_host="DH10B"
/note="Site 1: Sall; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN, Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGATCTGATTTTATTTTNN 3']. cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 185.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGATCTGATTTTATTTTATTTATCCCCCCCC 3']. cDNA was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda phage I."

BASE COUNT 48 a 57 c 52 g 57 t
ORIGIN

Query Match 23.2%; Score 88; DB 9; Length 214;
Best Local Similarity 90.4%; Pred. No. 2.3e-15;
Matches 94; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 3 AAGCAGACAGCTGCTCCGGCTCAGAGCATTCGGCGAGTGTCCCGTGAATGC 62
|||||
Db 6 AGGCACAAGCTGCTCCGGGTCCAAAGATTCGGCGGAAATGTTCCCGTGAATGC 65
|||||
QY 63 TCCATCACTGACTGCTCATCATCTCTGCTGCTGCTGCTCCCT 106
|||||
Db 66 TCCATCACTGACTGCTCATCATCTCTGCTGCTGCTGCTCCCT 109
|||||

RESULT 14
AA038641 257 bp mRNA linear EST 28-AUG-1996
LOCUS
DEFINITION m194a06.r1 Soares mouse p3NM19.5 Mus musculus cDNA clone

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

IMAGE:474226.5' similar to SW:LOX5_RAT P12527 ARACHIDONATE
5-LIPOXYGENASE ; mRNA sequence.

AA038641
AA038641.1 GI:1514164

REFERENCE

1 (bases 1 to 257)
Marta, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kuwaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.
The WashU-HMNI Mouse EST Project
Unpublished (1996)
Contact: Marta M/Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810

TITLE

JOURNAL

WashU-HMNI Mouse EST Project

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810

Email: mouseest@wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
MGI:284970

Possible reversed clone: similarity on wrong strand
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 219.

FEATURES

SOURCE

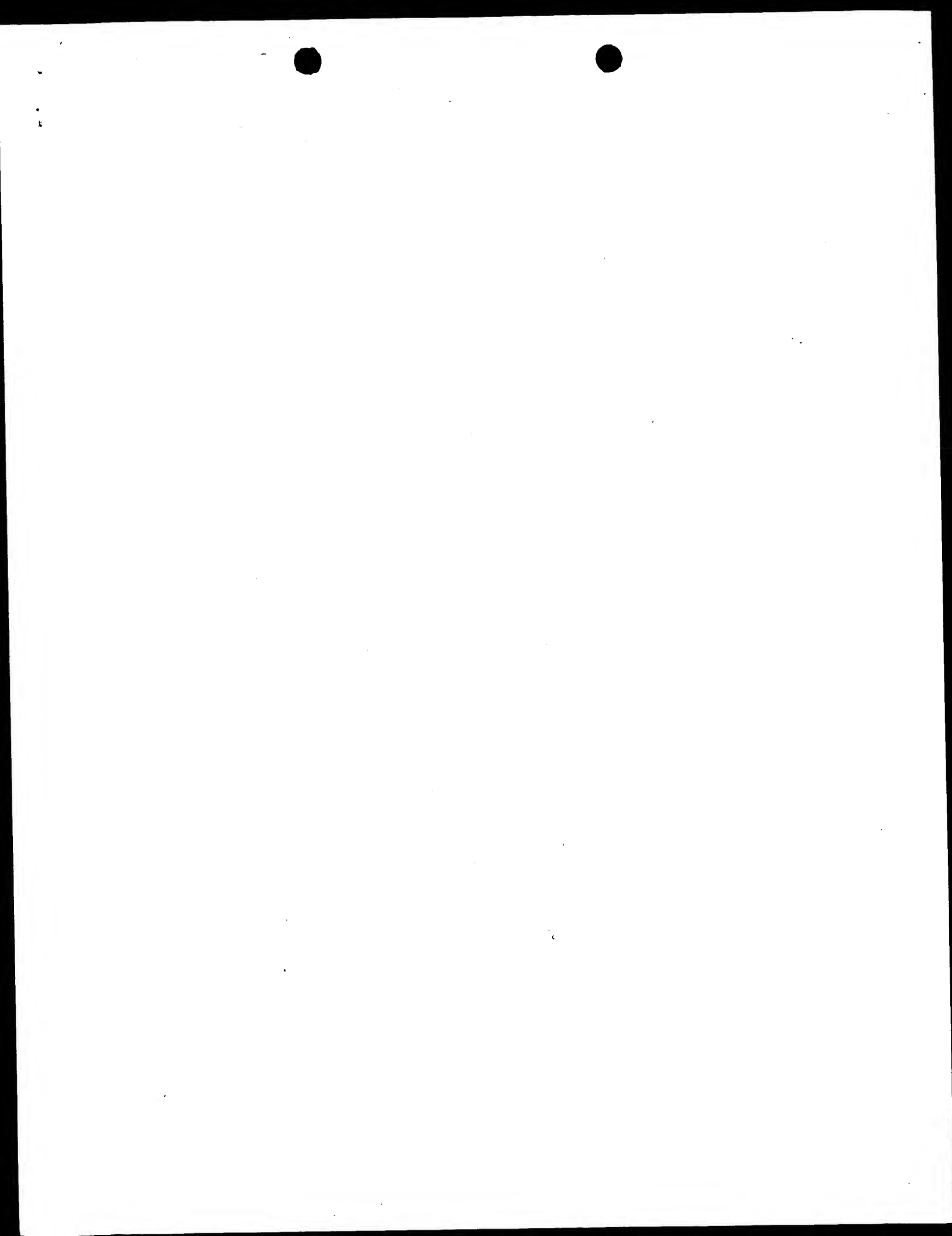
1. .257
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:474226"
/clone_11b="Soares mouse p3NM19.5"
/dev_stage="19.5 dpc total fetus"
/lab_host="DH10B (ampicillin resistant)"
/note="Vector: pT73D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - 0190(dT) primer [5' TGTACCAATCTGAGTGGAGGCGGCGGATTTTATTTT 3']. double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M. Fatima Bonaldo. RNA was kindly provided by Dr. Minoru Ko (Wayne State University)."

BASE COUNT 59 a 64 c 75 g 59 t
ORIGIN

Query Match 21.2%; Score 80.4; DB 9; Length 257;
Best Local Similarity 97.9%; Pred. No. 4.2e-13;
Matches 92; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 283 ACCCTCCGCGATATTTCGTATGACAGCTGGCGTGTGACCGATGAGAGCT 342
|||||
Db 1 ACCCTCCGCGATATTTCGTATGACAGCTGGCGTGTGACCGATGAGAGCT 60
|||||
QY 343 ACCTGACTAGAGATCATCTATTATTATCAAA 376
|||||
Db 61 ACCTGAC-AGAGATCATCTATTATTATCAAA 93
|||||

RESULT 15
A1385442 449 bp mRNA linear EST 27-JAN-1999
LOCUS
DEFINITION m194a06.y1 Soares mouse p3NM19.5 Mus musculus cDNA clone
IMAGE:474226.5' similar to TR:015296 O15296 15S-LIPOXYGENASE ; mRNA sequence.
ACCESSION A1385442



GenCore version 4.5
Copyright (c) 1993 - 2000 Compen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 24, 2002, 18:53:03 ; Search time 62.9 seconds
(without alignments)
1483.954 Million cell updates/sec

Title: W36511

Perfect score: 380
Sequence: 1 GCAGGCGACGACGCTGCTCC.....ACTTATTATTACCAATGAC 380

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database : Issued Patents, NA: *
1: /cgn2_6/ptodata/1/ina/5A.COMB.seq: *
2: /cgn2_6/ptodata/1/ina/5B.COMB.seq: *
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq: *
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq: *
5: /cgn2_6/ptodata/1/ina/PCITUS.COMB.seq: *
6: /cgn2_6/ptodata/1/ina/backfile1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	135.8	35.7	2469	US-09-087-727-1	Sequence 1, Appli
2	50	13.2	2685	US-09-061-768A-1	Sequence 1, Appli
3	50	13.2	3205	US-09-061-768A-3	Sequence 3, Appli
4	33.4	8.8	2124	US-09-198-122-1	Sequence 1, Appli
5	33.2	8.7	20235	US-07-642-734C-3	Sequence 3, Appli
6	33.2	8.7	20235	US-08-439-009A-3	Sequence 3, Appli
7	32.4	8.5	2049	US-09-099-749-10	Sequence 10, Appli
8	30.8	8.1	3271	US-08-852-806-1	Sequence 1, Appli
9	30.8	8.1	3271	US-09-163-669-1	Sequence 1, Appli
10	30	7.9	3710	US-07-741-453A-62	Sequence 62, Appli
11	29.8	7.8	2297	US-08-484-493-1	Sequence 1, Appli
12	29.8	7.8	2297	US-08-484-494-1	Sequence 1, Appli
13	29.8	7.8	2297	US-08-345-212-1	Sequence 1, Appli
14	29.8	7.8	2297	US-09-249-003-1	Sequence 1, Appli
15	29.8	7.8	3357	US-08-726-214-7	Sequence 7, Appli
16	29.4	7.7	1598	US-08-211-682-24	Sequence 24, Appli
17	29	7.6	411529	US-09-103-840A-1	Sequence 1, Appli
18	28.8	7.6	586	US-08-385-590A-3	Sequence 3, Appli
19	28.8	7.6	586	US-09-021-520-3	Sequence 3, Appli
20	28.8	7.6	31571	US-08-323-443B-1	Sequence 1, Appli
21	28.8	7.6	53526	US-08-658-136-2	Sequence 2, Appli
22	28.8	7.6	53577	US-08-658-136-2	Sequence 2, Appli
23	28.4	7.5	2968	US-09-813-819-1	Sequence 1, Appli
24	28.4	7.5	2968	US-09-920-048-1	Sequence 1, Appli
25	28.4	7.5	49377	US-08-764-233A-1	Sequence 1, Appli
26	28	7.4	1225	US-08-829-110-4	Sequence 4, Appli
27	28	7.4	28958	US-08-258-261B-6	Sequence 6, Appli

C	28	7.4	28958	1	US-08-456-837-6	Sequence 6, Appli
C	29	28	28958	1	US-08-457-342-6	Sequence 6, Appli
C	30	28	28958	1	US-08-457-342-6	Sequence 6, Appli
C	31	28	28958	1	US-08-457-342-6	Sequence 6, Appli
C	32	28	28958	1	US-08-457-342-6	Sequence 6, Appli
C	33	28	28958	1	US-08-457-342-6	Sequence 6, Appli
C	34	28	28958	1	US-08-457-342-6	Sequence 6, Appli
C	35	28	28958	1	US-08-457-342-6	Sequence 6, Appli
C	36	27.8	198	2	US-08-588-258B-22	Sequence 22, Appli
C	37	27.8	198	2	US-08-588-258B-22	Sequence 22, Appli
C	38	27.8	198	2	US-08-588-258B-22	Sequence 22, Appli
C	39	27.6	2291	2	US-08-476-062A-53	Sequence 53, Appli
C	40	27.4	1945	1	US-08-724-194-1	Sequence 1, Appli
C	41	27.4	2678	1	US-08-724-194-2	Sequence 2, Appli
C	42	27.4	3933	1	US-08-199-776-1	Sequence 1, Appli
C	43	27.4	3933	3	US-08-663-731-1	Sequence 1, Appli
C	44	27.4	3933	3	US-08-879-338-1	Sequence 1, Appli
C	45	27.4	3933	5	PCT-US95-02044-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-087-727-1
; Sequence 1, Application US/09087727A
; Patent No. 6103496
; GENERAL INFORMATION:
; APPLICANT: Brash, Alan R
; APPLICANT: Boeglin, William E
; APPLICANT: Kim, Richard B
; TITLE OF INVENTION: Isolated and Purified 12R-Lipoxygenase Protein and
; FILE REFERENCE: Attorney Docket No. 6103496 1242-7
; CURRENT APPLICATION NUMBER: US/09/087,727A
; CURRENT FILING DATE: 1996-05-29
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2469
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (260)..(2362)
US-09-087-727-1

Query Match 35.7%; Score 135.8; DB 3; Length 2469;
Best Local Similarity 83.4%; Pred. No. 4.2e-36;
Matches 166; Conservative 0; Mismatches 32; Indels 1; Gaps 1;

QY 175 TTTCCTGGGCTTGGAGGCTTCCACAGGTGATGCTTCCGCTCTGAGCTACCT 234
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DB 1686 atgcagcctctactctcccaatgactcttggtggcggtccagagccctggat 1745
QY 295 ATATTTTCCTGATGACGCTTTCGAGCGCGGCTTTCGAGCGGTGAGAGCTAGTAC 354
DB 1746 attactaccgcgcatgacagcttggtggcggtccagagccctggat 1804
QY 355 ATCATCTATTATTATTC 373
DB 1805 atcatcattattatc 1823

RESULT 2
US-09-061-768A-1
; Sequence 1, Application US/09061768A
; Patent No. 6204037

GENERAL INFORMATION:
APPLICANT: BRASH, ALAN R.
APPLICANT: BOEGLIN, WILLIAM E.
APPLICANT: JISAKA, MITSUO
TITLE OF INVENTION: LIPOXYGENASE PROTEINS AND NUCLEIC ACIDS
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: ARLES A. TAYLOR, JR.
STREET: SUITE 1400, UNIVERSITY TOWER, 3100 TOWER BOULEVARD
CITY: DURHAM
STATE: NORTH CAROLINA
COUNTRY: USA
ZIP: 27707
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4 MB storage
COMPUTER: IBM PC/XT/AT compatible
OPERATING SYSTEM: Windows 3.1
SOFTWARE: WORD PERFECT 6.1 and ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/061,768A
FILING DATE: APRIL 16, 1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA: NONE
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: ARLES A. TAYLOR, JR.
REGISTRATION NUMBER: 39,395
REFERENCE/DOCKET NUMBER: 1242/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 493-8000
TELEFAX: (919) 419-0383
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2685 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
US-09-061-768A-1

Query Match 13.2%; Score 50; DB 4; Length 2685;
Best Local Similarity 56.6%; Pred. No. 4.4e-07;
Matches 112; Conservative 0; Mismatches 85; Indels 1; Gaps 1;

QY 179 CTTGGGCTAGAGGCTTCGACAGATGATGTTGGGGTCTGTCGAGCTACCTACAA 238
DB 1367 CATGGGATTGAAGGCTTCTGTGATGATACAGAGACATGAAGCAGCTGACTATTC 1426
DB 239 AAGCCTCTGATTCACACGACTTTGTGAGCGCGGGTCCAGAGCTGCTGGGTATTA 298
DB 1427 TCTCTGTGTCTGCTGATGATATCCGACCCGAGGATGGAAGACATCCAGGCTACTA 1486
QY 299 TTTCCGATGACAGCTGGCGGTGTGTACCGGATGGAAGTACGTACTGAGATCA 358
DB 1487 CTACCGATGATGGGATGAGATTTGGGGTGGAGCGCTTGTCTCT-GAATCA 1545
QY 359 TCACCTATTATTACCAAA 376
DB 1546 TCGGATCTACTACCA 1563

RESULT 3
US-09-061-768A-3
Sequence 3, Application US/09061768A
GENERAL INFORMATION:
APPLICANT: BRASH, ALAN R.
APPLICANT: BOEGLIN, WILLIAM E.
APPLICANT: JISAKA, MITSUO
TITLE OF INVENTION: LIPOXYGENASE PROTEINS AND NUCLEIC ACIDS
NUMBER OF SEQUENCES: 36

CORRESPONDENCE ADDRESS:
ADDRESSEE: ARLES A. TAYLOR, JR.
STREET: SUITE 1400, UNIVERSITY TOWER, 3100 TOWER BOULEVARD
CITY: DURHAM
STATE: NORTH CAROLINA
COUNTRY: USA
ZIP: 27707
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4 MB storage
COMPUTER: IBM PC/XT/AT compatible
OPERATING SYSTEM: Windows 3.1
SOFTWARE: WORD PERFECT 6.1 and ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/061,768A
FILING DATE: APRIL 16, 1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA: NONE
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: ARLES A. TAYLOR, JR.
REGISTRATION NUMBER: 39,395
REFERENCE/DOCKET NUMBER: 1242/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 493-8000
TELEFAX: (919) 419-0383
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3205 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
US-09-061-768A-3

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Best Local Similarity 53.0%; Pred. No. 4.8e-07;
Matches 107; Conservative 0; Mismatches 95; Indels 0; Gaps 0;

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DB 1359 TCTCTGTGTCTGCTGATGATATCCGACCCGAGGATGGAAGACATCCAGGCTACTA 1418
QY 299 TTTCCGATGACAGCTGGCGGTGTGTACCGGATGGAAGTACGTACTGAGATCA 358
DB 1419 TTACCGATGATGGGATGAGATCTGGGGGATGGAAGCTTGTCTGAAATAGT 1478
QY 359 TCACCTATTATTACCAATGAC 380
DB 1479 CAGCATCTACTATCCAAAGTAC 1500

RESULT 4
US-09-198-122-1
Sequence 1, Application US/09198122
Patent No. 6180380
GENERAL INFORMATION:
APPLICANT: Strebhardt, Klaus; Rubsamen-Waligmann, Helga;
APPLICANT: Holtrich, Uwe
TITLE OF INVENTION: CLONING OF A MEMBER OF THE SERINE-
NUMBER OF SEQUENCES: 7
TITLE OF INVENTION: THREONINE-KINASE FAMILY
CORRESPONDENCE ADDRESS:
ADDRESSEE: SPRUNG HORN KRAMER & WOODS
STREET: 660 White Plains Road
CITY: Tarrytown
STATE: New York
COUNTRY: U.S.A.

ZIP: 10591-5144
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 2.0 MB
MEDIUM TYPE: storage
COMPUTER: NEC Powermate SX-20
OPERATING SYSTEM: DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/198,122
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/601,014
FILING DATE: 23-FEB-1996
APPLICATION NUMBER: PCT/EP94/02863
FILING DATE: 30-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4329177
FILING DATE: 30-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Kurt G. Briscoe
REGISTRATION NUMBER: 33,141
REFERENCE/DOCKET NUMBER: Bayer 9516-KGB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 332-1700
TELEFAX: (914) 332-1844
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2124 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ANTI-SENSE: yes
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 65..1873
US-09-198-122-1

Query Match 8.8%; Score 33.4; DB 4; Length 2124;
Best Local Similarity 58.6%; Pred. No. 0.16;
Matches 58; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

225 GAGCTACCTACGAAAGCCCTGTCATCCCAAGACTTTGTGGAGCGGGGTCCAGGAC 284
1268 GATCCGTCGCTGATCCCACTCTGTGGTCAGCAAGTGGGTGACTATTTCGGCAAGTAC 1327

285 CTGCTGGGTATTTTCGATGACAGCGCGGGGTG 323
1328 GGCCTTGGGTATCAAGCTCTGTGTATTAACAGCGTGGGGTG 1366

Db 1328 GGCCTTGGGTATCAAGCTCTGTGTATTAACAGCGTGGGGTG 1366

RESULT 5
US-07-642-734C-3/C
Sequence 3, Application US/07642734C
Patent No. 5824513
GENERAL INFORMATION:
APPLICANT: Katz, L
APPLICANT: Donadio, S
APPLICANT: McAlpine, J B
TITLE OF INVENTION: Recombinant DNA Method for Producing
TITLE OF INVENTION: Erythromycin Analogs
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Edward H. Gorman
STREET: Abbott Laboratories D377/AP6D-2 One Abbott
CITY: Abbott Park
STATE: IL

COUNTRY: US
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/642,734C
FILING DATE: 17-JAN-91
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Danckers, Andreas M
REGISTRATION NUMBER: 32652
REFERENCE/DOCKET NUMBER: 4952 US 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-9396
TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 20235 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Saccharopolyspora erythraea
STRAIN: NRRL 238
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NAME/KEY: CDS
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OTHER INFORMATION: 6-deoxyerythronolide B"
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NAME/KEY: misc_feature

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US-07-642-734C-3

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Query Match      8.7%; Score 33.2; DB 1; Length 20235;
Best Local Similarity 52.1%; Pred. No. 0.59;
Matches 74; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

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QY 189 GAGGCTTCGACAGTATGTTGGGGTCTGTGAGCTCACCCTACAAAGCTCTGC 248
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DB 17682 GAGCTGGGATGATCTCTCCGCGGTGCGGTGACGACACCGAGTGGCAGGC 17623
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QY 249 ATTCCACGACTTGTGAGCGCGGGGTCCAGACCTGCTGGATATTATTCGTGAT 308
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DB 17622 GTCCCGGCGATCTCTGACCGCGCGGTGAGCAGCAGCGGATCATCTGAGGAA 17563
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QY 309 GACAGCTGGCGGTGTGTACG 330
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RESULT 6
US-08-439-009A-3/c
; Sequence 3, Application US/08439009A
; Patent No. 6004787
; GENERAL INFORMATION:
; APPLICANT: Donadio, S
; APPLICANT: Katz, L
; TITLE OF INVENTION: Method of Directing Biosynthesis of
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESS: Steven F. Weinstein
; STREET: Abbott Laboratories D377/APD-2 One Abbott
; CITY: Abbott Park
; STATE: IL
; COUNTRY: US
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/439,009A
; FILING DATE: 11-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Casuto, Dianne
; REGISTRATION NUMBER: 40,943
; REFERENCE/DOCKET NUMBER: 4952.US.D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847-938-3137
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20235 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEetical: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Saccharopolyspora erythraea

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NAME/KEY: CDS
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OTHER INFORMATION: /product= "eryA ORF2 encoding modules 3 & 4 for
OTHER INFORMATION: 6-deoxyerythronolide B"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 19..4470
OTHER INFORMATION: /function= "approximate span of
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NAME/KEY: misc_feature
LOCATION: 97..1482
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OTHER INFORMATION: beta-ketoacyl ACP synthase of module 3"
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NAME/KEY: misc_feature
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LOCATION: 14062..14610
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US-08-439-009A-3

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Query Match      8.7%; Score 33.2; DB 3; Length 20235;
Best Local Similarity 52.1%; Pred. No. 0.59;
Matches 74; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

QY 189 GAGGCTTCGACAGGTGATGGTTGGGGTCTGCTGAGCTCAGCTACGAAAGCCTCTGC 248
DB 17682 GAGCTGGGCGATGAGTGTCTCCGCGGTGTCGGGTGACGACGACCGGATGGCGACGGC 17623

QY 249 ATCCCAAGCACTTGTGGAGCGGCGGTCGACGACGACGCTGCTGATATTATTCCTGAT 308
DB 17622 GTCCGGGGGATCTCTGACCGCGCGGTGAGCACGCGGTGCGGGCTCATCTGACGAA 17563

QY 309 GACAGCTTGCGGCTGTGTACG 330
DB 17562 GGTGGCTGACCGTGGCGACG 17541

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RESULT 7

US-09-099-749-10
; Sequence 10, Application US/09099749B
; Patent No. 6306591
; GENERAL INFORMATION:
; APPLICANT: Utah State University
; TITLE OF INVENTION: Screening For The Molecular Defect Causing Spider Lamb
; FILE REFERENCE: 370605
; CURRENT APPLICATION NUMBER: US/09/099,749B
; CURRENT FILING DATE: 1998-06-18
; EARLIER APPLICATION NUMBER: 60/050,127
; EARLIER FILING DATE: 1997-06-18
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Corel Wordperfect 8.0
; SEQ ID NO 10
; LENGTH: 2049
; TYPE: DNA
; ORGANISM: Sheep
US-09-099-749-10

Query Match 8.5%; Score 32.4; DB 4; Length 2049;
Best Local Similarity 55.3%; Pred. No. 0.34; Mismatches 0; Gaps 0;
Matches 63; Conservative 0; Indels 51; Indels 0; Gaps 0;

QY 226 AGCTACCTACCAAGACCTGTCATTCCTCCAGACATTGTCGAGCGCGGCTCCAGAGACC 285
DB 1383 agctaccttcaagacctgtgtctcgtaccagtgctgctgagcagtgatgagc 1442
QY 286 TGCCGTGGGTATTATTCGCTGATGACACACCGCGGCTGTGTAGCGCATGGAGA 339
DB 1443 tggccctcgagagatgcatccatagagacctgctgagcccgacagctgctgagc 1496

RESULT 8
US-08-852-806-1/c
; Sequence 1, Application US/08852806
; Patent No. 5874245
; GENERAL INFORMATION:
; APPLICANT: Shoji Fukusumi
; APPLICANT: Shuji Hinuma
; TITLE OF INVENTION: NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Smithkline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/852,806
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/017,915
; FILING DATE: 16 MAY 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Han, William T
; REGISTRATION NUMBER: 34,344
; REFERENCE/DOCKET NUMBER: TAK50002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5219
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3271 base pairs

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
US-08-852-806-1

Query Match 8.1%; Score 30.8; DB 2; Length 3271;
Best Local Similarity 66.7%; Pred. No. 1.5;
Matches 44; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 4 AGGACGAGCTGCTCCCGCTCCAGAGACATTGCGGAGACAGTGTCCGCTGACTGCT 63
DB 239 AGACAGCGCGGCTGCGACGACCTGAGGCACTTGTGGGGCAGCTTGTAGATGATCTCG 180
QY 64 CCATCA 69
DB 179 CCAGCA 174

RESULT 9
US-09-163-669-1/c
; Sequence 1, Application US/09163669
; Patent No. 611076
; GENERAL INFORMATION:
; APPLICANT: FUKUSUMI, SHOJI
; APPLICANT: FUJII, RYO
; APPLICANT: HINUMA, SHUJI
; TITLE OF INVENTION: NOVEL HUMAN G-PROTEIN COUPLED
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ratner & Prestlia
; STREET: P.O. Box 980
; CITY: Valley Forge
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/163,669
; FILING DATE: 30-SEP-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/852,806
; FILING DATE: 07-MAY-1997
; APPLICATION NUMBER: 60/017,915
; FILING DATE: 16-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Prestlia, Paul F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: TAK-50002-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0700
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3271 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-09-163-669-1

Query Match
Best Local Similarity 8.1%; Score 30.8; DB 3; Length 3271;
Matches 44; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 4 AGGAGAGCGTCCCGGCTCCAGAGGCACTTCCGCGAGAGTGTCCCGCTGACTGCT 63
DB 239 AGACAGCGGCGGCTGCGACAGCCTGAGGCACTTGGGGGCGGCTGTGATGATCTCG 180
QY 64 CCATCA 69
DB 179 CCAGCA 174

RESULT 10
-US-07-741-453A-62

Sequence 62, Application US/07741453A
Patent No. 6228597

GENERAL INFORMATION:

APPLICANT: PARMENTIER, MARC

APPLICANT: LIBERT, FREDERIC

APPLICANT: DIMONT, JACQUES

APPLICANT: VASSART, GILBERT

TITLE OF INVENTION: POLYPEPTIDES HAVING THYROTROPIN-RECEPTOR

TITLE OF INVENTION: ACTIVITY, NUCLEIC ACID SEQUENCES CODING FOR SUCH RECEPTORS

NUMBER OF SEQUENCES: 62

CORRESPONDENCE ADDRESS:

ADDRESSEE: CUSHMAN DARBY & CUSHMAN

STREET: 1615 L STREET, N.W.

CITY: WASHINGTON, D.C.

COUNTRY: U.S.A.

ZIP: 20036

COMPUTER READABLE FORM:

MEDIUM TYPE: Disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/741.453A

FILING DATE: 19911015

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: KOKULIS, PAUL N.

REGISTRATION NUMBER: 16773

REFERENCE/DOCKET NUMBER: 91913/1107/US/ST

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 861-3000

TELEFAX: (202) 822-0944

INFORMATION FOR SEQ ID NO: 62:

SEQUENCE CHARACTERISTICS:

LENGTH: 3710 base pairs

TYPE: NUCLEIC ACID

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

US-07-741-453A-62

Query Match
Best Local Similarity 7.9%; Score 30; DB 4; Length 3710;
Matches 78; Conservative 0; Mismatches 80; Indels 0; Gaps 0;

QY 46 TGGTCCGCTGAGCTGCTCCATCATGACTGCTGCATCATGCTGCTGCTGCTGCC 105
DB 126 TGGCTTCCCTCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 185
QY 106 TGGTCCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 165
DB 186 TTTCTCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 245
QY 166 TAAGAAATATTTTCCCTGAGGCTAGAGGCTTGCACAG 203

DB 246 CTGAAATGTGTTCTCTCCCGAGGCGGAGGCTGAG 283

RESULT 11
US-08-484-493-1

Sequence 1, Application US/08484493
Patent No. 5728381

GENERAL INFORMATION:

APPLICANT: Wilson, Peter J

APPLICANT: Morris, Charles P

APPLICANT: Anson, Donald S

APPLICANT: Occhiodoro, Teresa

APPLICANT: Bielecki, Julie

APPLICANT: Clements, Peter R

APPLICANT: Hopwood, John J

TITLE OF INVENTION: GLYCOSYLATION VARIANTS OF

TITLE OF INVENTION: IDURONATE 2-SULFATASE

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSEE: Scully, Scott, Murphy & Presser

STREET: 400 Garden City Plaza

CITY: Garden City

STATE: New York

COUNTRY: USA

ZIP: 11530

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/484.493

FILING DATE: 07-JUN-1995

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 991,973

FILING DATE: 17-DEC-1992

ATTORNEY/AGENT INFORMATION:

NAME: Digilio, Frank S

REGISTRATION NUMBER: 31,346

REFERENCE/DOCKET NUMBER: 84162

TELECOMMUNICATION INFORMATION:

TELEPHONE: 516-742-4343

TELEFAX: 516-742-4366

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 2297 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 125..1774

US-08-484-493-1

Query Match
Best Local Similarity 7.8%; Score 29.8; DB 1; Length 2297;
Matches 70; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

QY 177 TCCCTGGGCTAGAGGCTTCCGACAGGATGATGCTGCGGCTGCTGAGCTCAGCTAC 236
DB 272 TCCCTGGGCTAGAGGATAGAGTGTGAGGCTGCCCAATATGACCACTGCGATCC 331
QY 237 AAAAGCTCTGCAATCCCAAGCACTTTGTGAGCGCGGCTCCAGAGCTGCTGGGAT 296
DB 332 CACAGCTCTCTCCAGATGCTTTGGGAGCAAGCAAGTGTGGCGCCGAGCGGCTT 391
QY 297 TATTCCTGATGACAG 313

RESULT 14
US-09-249-003-1

; Sequence 1, Application US/09249003

; Patent No. 6153188

GENERAL INFORMATION:

; APPLICANT: Wilson, Peter J

; APPLICANT: Morris, Charles P

; APPLICANT: Anson, Donald S

; APPLICANT: Occhiodoro, Teresa

; APPLICANT: Bielicki, Julie

; APPLICANT: Clements, Peter R

; APPLICANT: Hopwood, John J

; TITLE OF INVENTION: GLYCOSYLATION VARIANTS OF

; TITLE OF INVENTION: IDURONATE 2-SULFATASE

; NUMBER OF SEQUENCES: 15

; CORRESPONDENCE ADDRESSES:

; ADDRESSEE: Scully, Scott, Murphy & Presser

; STREET: 400 Garden City Plaza

; CITY: Garden City

; STATE: New York

; COUNTRY: USA

; ZIP: 11530

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/249,003

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/991,973

; FILING DATE: 17-DEC-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Disigilio, Frank S

; REGISTRATION NUMBER: 31,346

; REFERENCE/DOCKET NUMBER: 84162

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 516-742-4343

; TELEFAX: 516-742-4366

; TELETYPE: 230 901 SANS UR

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 2297 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 125..1774

; US-09-249-003-1

Query Match 7.8%; Score 29.8; DB 3; Length 2297;
Best Local Similarity 51.1%; Pred. No. 2.8; Mismatches 67; Indels 0; Gaps 0;

Matches 70; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

QY 177 TCCTTGGGCTTGAAGGCTTGCACAGTGTGCGGGGTCTGTGAGCTACCTAC 236
DB 272 TCCTTGGGCTTGAAGGCTTGCACAGTGTGCGGGGTCTGTGAGCTACCTAC 236
QY 237 AAAGGCTTGCATTCACAGCTTTGTGAGCGCGGGGTCTGCAGAGCTCTGGGTAT 296
DB 332 CAAGGCTTCTCTTCAGAGTCCCTTGGCGAGCAAGCATGTGGCGCCCGAGCGGCTT 391
QY 297 TATTTCGGTATGACAG 313
DB 392 TCTTTCCTCATGTCGAG 408

RESULT 15
US-08-726-214-7

; Sequence 7, Application US/08726214

; Patent No. 6107076

GENERAL INFORMATION:

; APPLICANT: Tang, Wei-Jen

; APPLICANT: Gilman, Alfred G.

; TITLE OF INVENTION: SOLUBLE MAMMALIAN ADENYLYL CYCLASE

; TITLE OF INVENTION: AND USES THEREFOR

; NUMBER OF SEQUENCES: 31

; CORRESPONDENCE ADDRESSES:

; ADDRESSEE: Arnold, White & Durkee

; STREET: P.O. Box 4433

; CITY: Houston

; STATE: Texas

; COUNTRY: United States of America

; ZIP: 77210

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US 60/005,498

; FILING DATE: 04-OCT-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Highlander, Steven L.

; REGISTRATION NUMBER: 37,642

; REFERENCE/DOCKET NUMBER: UTSD:450

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (512) 474-7577

; TELEFAX: (512) 418-3000

; INFORMATION FOR SEQ ID NO: 7:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 3357 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

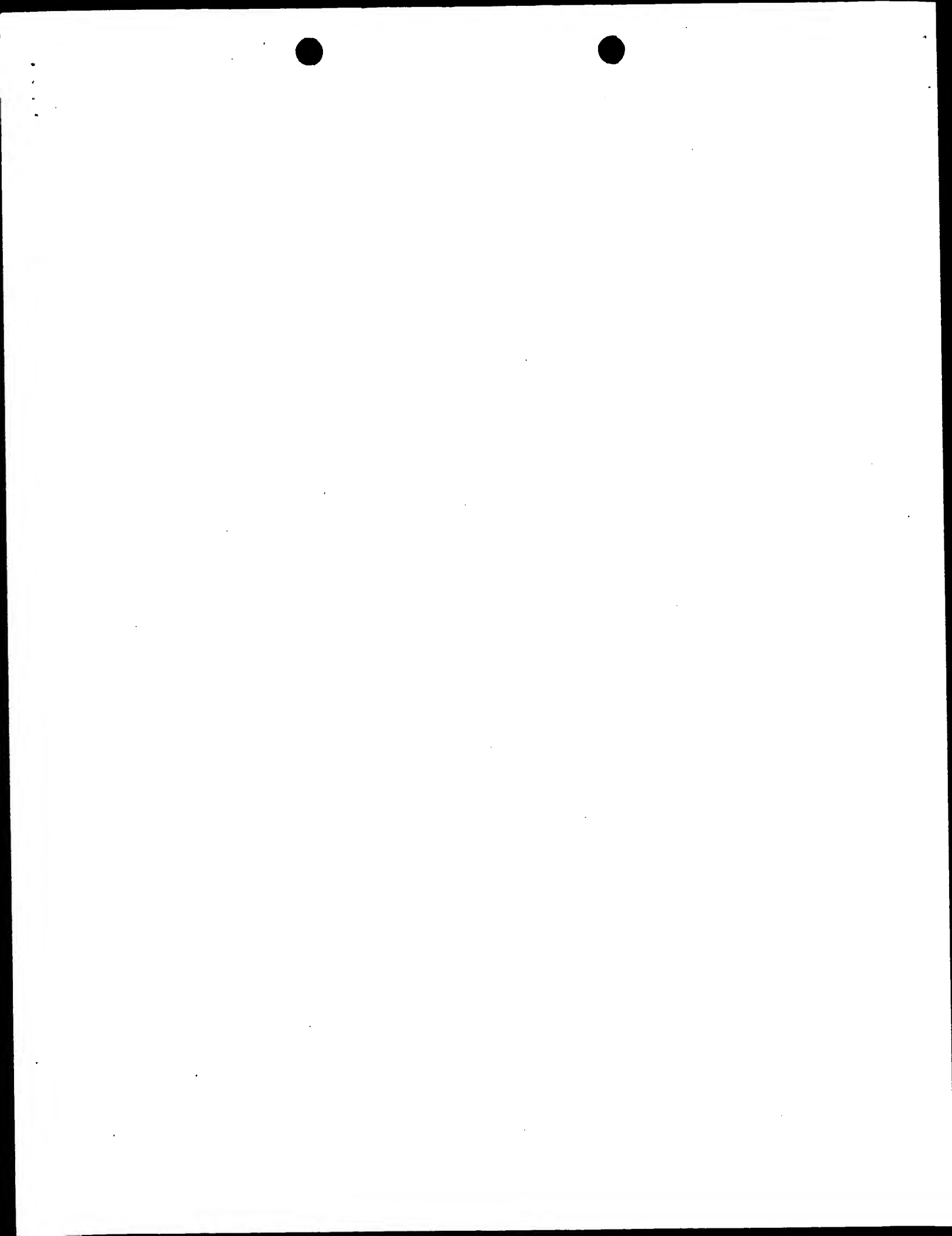
; US-08-726-214-7

Query Match 7.8%; Score 29.8; DB 3; Length 3357;
Best Local Similarity 50.3%; Pred. No. 3.3; Mismatches 72; Indels 0; Gaps 0;

Matches 73; Conservative 0; Mismatches 72; Indels 0; Gaps 0;

QY 180 CTGGGCTTGAAGGCTTGCACAGTGTGCGGGGTCTGTGAGCTACCTACAA 239
DB 962 CTGGGCTTGAAGGCTTGCACAGTGTGCGGGGTCTGTGAGCTACCTACAA 1021
QY 240 AGCTTGTGATTCACAGCTTTGTGAGCGCGGGGTCTGCAGAGCTCTGGGTAT 299
DB 1022 TTGACCAATATGCAAGAGGAGCAAGATGCATGCGATCAAGATCTCTGGAGACTGTAC 1081
QY 300 TTGCGTATGACAGCTCTGGCGGTGT 324
DB 1082 TACTGTGTATTCGGGCTGCTCTCT 1106

Search completed: May 25, 2002, 00:52:16
Job time: 21553 sec



GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: May 24, 2002, 23:55:26 ; Search time 315.63 Seconds
(without alignments)
2067.064 Million cell updates/sec

Title: w36511
Sequence: 1 GCAAGCAGCAGCTGCTCC.....ACTATATATACCAATGAC 380

Scoring table:
IDENTITY_NDC
Gapop 10.0 , Gapext 1.0

Number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
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23: /net/abs06/SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA2001B.DAT:*
24: /net/abs06/SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	135.8	35.7	2469	21	AAA59659
2	55.2	14.5	588	21	AAC61756
3	55.2	14.5	1383	21	AAC61752
4	55.2	14.5	1441	21	AAC61753
5	55.2	14.5	1848	21	AAC61751
6	55.2	14.5	2236	21	AAC61749
7	55.2	14.5	2316	21	AAC61760
8	55.2	14.5	2604	21	AAC61758
9	55.2	14.5	2701	21	AAC61747

10	55.2	14.5	3320	24	ABA05868	Human lipoxigenase
11	55.2	14.5	3384	21	AAC61761	CDNA encoding a hu
12	50	13.2	2647	20	AAK23827	Human 15S lipoxige
13	50	13.2	2685	22	AAD04501	Human 15S-lipoxye
14	50	13.2	3232	22	AAD04502	Mouse 8S-lipoxigen
15	44.6	11.7	2343	21	AAC58018	Arachidonic acid m
16	42	11.1	1000	21	AAC57997	Arachidonic acid m
17	42	11.1	20674	21	AAC58017	Arachidonic acid m
18	36.8	9.7	1980	23	AAC67977	CDNA encoding novel
19	35.2	9.3	1819	22	AAF30436	Rice apoptosis ind
20	33.4	8.8	2131	16	AAO88155	Human lung tumour
21	33.4	8.8	3331	24	AA594875	Human DNA sequence
22	33.2	8.7	29879	14	AAO46806	eryA region of S...
23	32.8	8.6	1030	23	AA583105	Human immune/haema
24	32.8	8.6	32986	22	AAK69758	Human immune/haema
25	32.8	8.6	32986	22	AAK64629	Human immune/haema
26	32.4	8.5	2049	23	AAD21622	Sheep fibroblast g
27	31.6	8.3	426	23	AA568333	CDNA encoding novel
28	31.6	8.3	8564	21	AAC74783	Human OREX ORF38
29	31.6	8.3	68940	20	AAK57351	Human chromosome 6
30	31.4	8.3	1397	21	AAK99043	Human pancreatic c
31	31.2	8.2	1433	22	AA105194	Human reproductive
32	31.2	8.2	1491	23	AA591851	DNA encoding novel
33	31.2	8.2	1509	15	AAO64910	Thermus thermophil
34	31.2	8.2	4151	24	AA594773	Human DNA sequence
35	31.2	8.2	8971	22	AAH02885	Human shear stress
36	31	8.2	777	22	AAH07681	Human CDNA clone (
37	31	8.2	1439	22	AAH14914	Human immune/haema
38	30.8	8.1	462	22	AAK57133	Human G-protein co
39	30.8	8.1	3271	19	AAV00060	Human BA12 gene.
40	30.8	8.1	5412	20	AAK21356	Human gene express
41	30.6	8.1	300	20	AAI13388	Maize Jabi homolog
42	30.6	8.1	1080	22	AA55498	Osteoarthritis tis
43	30.6	8.1	2539	22	AAH23109	Human CDNA clone (
44	30.4	8.0	726	22	AAH07120	Pseudomonas aerugi
45	30.4	8.0	870	23	AA554205	

ALIGNMENTS

RESULT 1	AAA59659	standard; DNA: 2469 BP.
ID	AAA59659	
AC	AAA59659	
XX		
DT	14-NOV-2000	(first entry)
XX		
DE	DNA encoding a human 12R-lipoxygenase polypeptide.	
XX		
KW	Human; 12R-lipoxygenase; arachidonic acid; proliferate dermatosis;	
KW	12R-hydroxycyclooctatetraenoic acid; psoriasis; arachidonic acid metabolite;	
KW	ss.	
XX		
OS	Homo sapiens.	
XX		
FH	Key	Location/Qualifiers
FT	CDS	260..2365
FT		/tag= a
FT		/product= "12R-lipoxygenase"
XX		
PN	US6103496-A.	
PD	15-AUG-2000.	
XX		
PF	29-MAY-1998;	98US-0087727.
XX		
PR	29-MAY-1998;	98US-0087727.
XX		
PA	(UYVA-) UNIV VANDERBILT.	
XX		
PI	Brash AR, Kim RB, Boeglin WE.	

DR	XX	WPI: 2000-542551/49.
DR	P-PSDB:	AAB07775.
XX	Novel isolated and purified nucleic acids encoding human	
PT	12R-lipoxygenase protein useful as new target for therapy in psoriasis	
PS	-	
CC	Claim 3; Fig 2; 32pp; English.	
CC	The present sequence encodes a human 12R-lipoxygenase polypeptide.	
CC	The enzyme metabolises arachidonic acid to 12R-hydroxylcoastetraenoic	
CC	acid. The 12R-lipoxygenase polynucleotide is used as a probe or primer	
CC	and as a target in gene therapy methods for treating psoriasis and other	
CC	proliferate dermatoses which have accumulated levels of unusual	
CC	arachidonic acid metabolite in the skin. It is also used as diagnostic	
CC	tool to detect normal and abnormal DNA sequences in DNA derived from	
CC	patient cells, means for detecting and isolating other members of the	
CC	polypeptide family and related polypeptides from a DNA library	
CC	potentially containing such sequences, primers for hybridising,	
CC	to related sequences for the purpose of amplifying those sequences,	
CC	primers for altering native lipoxygenase DNA sequence.	
SQ	Sequence 2469 BP; 522 A; 808 C; 648 G; 491 T; 0 other;	
Query Match	35.7%; Score 135.8; DB 21; Length 2469;	
Best Local Similarity	83.4%; Pred. No. 6,5e-34;	
Matches 166; Conservative	0; Mismatches 32; Indels 1; Gaps 1	
OY	175 TTTCCTGGGCGCCAGAGGGCTTCCACAGGTGATGGTGCGGGTCTGTGAAGTTACCT 234	
Dd	1626 tgccttcgtggcgccgaggaaggccttgcggygtgatgtaagygctctgtggagctacct 1685	
OY	235 ACAAAAGCCTCTGCATTGCCAACGACTTTGTGGAGCGCGGGGTCCAGAGACTTCCTGGGT 294	
Dd	1686 atgacagcgccctaccctcccacaatgactttgtgagcgttg99gtccagagactgcttggat 1745	
OY	295 ATTATTCCGTGATGACAGCGCTGGCGGTGTGGTAACCGAATGGAGAGGTACGTAAGTAGAG 354	
Dd	1746 attactaacccgatagcagcttgcgcygtlgtgaagtcatcgcgagaagtatgtgac-g9ag 1804	
OY	355 ATCATCACTATTATTATACC 373	
Dd	1805 atcaatcacattatattacc 1823	
RESULT	2	
AAAC61756	AAAC61756 standard; cDNA; 588 BP.	
AAAC61756;		
XX	06-MAR-2001 (first entry)	
DE	cDNA encoding a human lipoxygenase protein.	
XX	Human; lipoxygenase; leukotriene; lipid; chemotactic agent;	
KW	Inflammation; smooth muscle contraction; asthma; eye disease; arthritis;	
KW	lung disease; cancer; acne; psoriasis; ss.	
OS	Homo sapiens.	
XX		
FH	Key Location/Qualifiers	
FT	CDS 1..588	
FT	/*tag= a	
FT	/product= "lipoxygenase"	
XX	WO200061765-A2.	
PN	19-OCT-2000.	
PD		
XX	12-APR-2000; 2000OWO-US09657.	

[illegible]

Sequence 1383 BP; 296 A; 432 C; 376 G; 279 T; 0 other;

PN WO200061765-A2

Sequence 1441 BP; 316 A; 492 C; 343 G; 290 T; 0 other;

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/product= "lipoxygenase"

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XX      WO200061765-A2.
XX      19-OCT-2000.
XX      12-APR-2000; 2000MO-US09657.
XX      12-APR-1999; 99US-0128817.
XX      24-AUG-1999; 99US-0150454.
XX      (LEXI-) LEXICON GENETICS INC.
XX      Turner CA, Zambrowicz B, Nehls M, Friedrich G, Sands AT;
XX      WPI: 2000-665134/64.
XX      P-PSDB: AAB19383.
XX      Novel polynucleotides encoding human lipoxigenase proteins useful for
XX      producing transgenic animals preferably mouse
XX      Claim 1; Page 65-66; 83pp; English.
XX
XX      AAC61747-60 encode novel human lipoxigenase proteins. Lipoxigenases
XX      oxidise lipids to produce leukotrienes. Leukotrienes bind cognate
XX      receptors and trigger biological effects. Leukotrienes influence a
XX      variety of biological processes, and can serve as, inter alia, potent
XX      chemotactic agents and mediators of inflammation, smooth muscle
XX      contractions, etc.. Lipoxigenases and leukotrienes are implicated in
XX      a variety of diseases and disorders, such as asthma, eye diseases,
XX      arthritis, lung disease, cancer, acne, psoriasis, etc..
XX      Sequence 1848 BP; 391 A; 568 C; 511 G; 378 T; 0 other:
XX
XX      Query Match      14.5%; Score 55.2; DB 21; Length 1848;
XX      Best Local Similarity 54.4%; Pred. No. 1.2e-07;
XX      Matches 111; Conservative 0; Mismatches 93; Indels 0; Gaps 0;
XX
XX      QY 177 TCCTGGGCTTAGAGGCTTCGACAGGTGATGTTGCGGGTCTGTGACTACCTAC 236
XX      1399 tccatcggaagcagagcccatctacatgagcagcggccttgcccatctac 1458
XX      237 AAAAGCCTCTGATTCCTCCACAGACTTTGTGAGCGCGGGCTCAGACCTGCTGGGAT 296
XX      1459 accaatcttcgcttcgagcagcctgcggccgcgcgtcctgctatccccaactac 1518
XX      QY 297 TATTTCCGATGATGACAGCTCGCGGTGTGTAGCGCATGAGAGTACGTAAGAT 356
XX      1519 cactaccgagacgagcgcctgaagatctcggcgccatcgagagcttctcagaatc 1578
XX      DB 357 CATCACTTATTATTACCAATGAC 380
XX      1579 gtggctactatctatcccgatgac 1602
XX
XX      RESULT 6
XX      AAC61749
XX      ID AAC61749 standard; cDNA; 2236 BP.
XX      AC AAC61749;
XX      DT 06-MAR-2001 (first entry)
XX      DE cDNA encoding a human lipoxigenase protein.
XX      KW Human; lipoxigenase; leukotriene; lipid; chemotactic agent;
XX      inflammation; smooth muscle contraction; asthma; eye disease; arthritis;
XX      lung disease; cancer; acne; psoriasis; ss.
XX      OS Homo sapiens.
XX      FT Key Location/Qualifiers
XX      CDS 1..1671

```

```

XX      /tag= a
XX      /product= "lipoxigenase"
XX      WO200061765-A2.
XX      19-OCT-2000.
XX      12-APR-2000; 2000MO-US09657.
XX      12-APR-1999; 99US-0128817.
XX      24-AUG-1999; 99US-0150454.
XX      (LEXI-) LEXICON GENETICS INC.
XX      Turner CA, Zambrowicz B, Nehls M, Friedrich G, Sands AT;
XX      WPI: 2000-665134/64.
XX      P-PSDB: AAB19381.
XX      Novel polynucleotides encoding human lipoxigenase proteins useful for
XX      producing transgenic animals preferably mouse
XX      Claim 1; Page 62; 83pp; English.
XX
XX      AAC61747-60 encode novel human lipoxigenase proteins. Lipoxigenases
XX      oxidise lipids to produce leukotrienes. Leukotrienes bind cognate
XX      receptors and trigger biological effects. Leukotrienes influence a
XX      variety of biological processes, and can serve as, inter alia, potent
XX      chemotactic agents and mediators of inflammation, smooth muscle
XX      contractions, etc.. Lipoxigenases and leukotrienes are implicated in
XX      a variety of diseases and disorders, such as asthma, eye diseases,
XX      arthritis, lung disease, cancer, acne, psoriasis, etc..
XX      Sequence 2236 BP; 493 A; 733 C; 555 G; 455 T; 0 other:
XX
XX      Query Match      14.5%; Score 55.2; DB 21; Length 2236;
XX      Best Local Similarity 54.4%; Pred. No. 1.3e-07;
XX      Matches 111; Conservative 0; Mismatches 93; Indels 0; Gaps 0;
XX
XX      QY 177 TCCTGGGCTTAGAGGCTTCGACAGGTGATGTTGCGGGTCTGTGACTACCTAC 236
XX      934 tccatcggaagcagagcccatctacatgagcagcggccttgcccatctac 993
XX      237 AAAAGCCTCTGATTCCTCCACAGACTTTGTGAGCGCGGGCTCAGACCTGCTGGGAT 296
XX      994 accaatcttcgcttcgagcagcctgcggccgcgcgtcccgccatccccaactac 1053
XX      QY 297 TATTTCCGATGATGACAGCTCGCGGTGTGTAGCGCATGAGAGTACGTAAGAT 356
XX      1054 cactaccgagacgagcgcctgaagatctcggcgccatcgagagcttctcagaatc 1113
XX      DB 357 CATCACTTATTATTACCAATGAC 380
XX      1114 gtggctactatctatcccgatgac 1137
XX
XX      RESULT 7
XX      AAC61760
XX      ID AAC61760 standard; cDNA; 2316 BP.
XX      AC AAC61760;
XX      DT 06-MAR-2001 (first entry)
XX      DE cDNA encoding a human lipoxigenase protein.
XX      KW Human; lipoxigenase; leukotriene; lipid; chemotactic agent;
XX      inflammation; smooth muscle contraction; asthma; eye disease; arthritis;
XX      lung disease; cancer; acne; psoriasis; ss.
XX      OS Homo sapiens.
XX      FT

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Key Location/Qualifiers
 CDS 1..2316
 /*tag= a
 /product= "lipoxigenase"

MO200061765-A2.

19-OCT-2000.

12-APR-2000; 2000MO-US09657.

12-APR-1999; 99US-0128817.

24-AUG-1999; 99US-0150454.

(LEXI-) LEXICON GENETICS INC.

Turner CA, Zambrowicz B, Nehls M, Friedrich G, Sands AT;

WPI: 2000-665134/64.

P-PSDB; AAB19392.

Novel polynucleotides encoding human lipoxigenase proteins useful for producing transgenic animals preferably mouse
 Claim 1; Page 79; 83pp; English.

AAC61747-60 encode novel human lipoxigenase proteins. Lipoxigenases oxidise lipids to produce leukotrienes. Leukotrienes bind cognate receptors and trigger biological effects. Leukotrienes influence a variety of biological processes, and can serve as, inter alia, potent chemotactic agents and mediators of inflammation, smooth muscle contractions, etc.. Lipoxigenases and leukotrienes are implicated in a variety of diseases and disorders, such as asthma, eye diseases, arthritis, lung disease, cancer, acne, psoriasis, etc..

Sequence 2316 BP; 486 A; 724 C; 651 G; 455 T; 0 other;

Query Match 14.5%; Score 55.2; DB 21; Length 2316;
 Best Local Similarity 54.4%; Pred. No. 1.3e-07;

Matches 111; Conservative 0; Mismatches 93; Indels 0; Gaps 0;

QY 177 TCCCTGGGCTAGAGGCTTGCACAGGTGATGGTTCGGGTCTGTGAGCTACCTAC 236
 1867 tccatcgaggaagagcctcatctactatgagcaagcgccgcccacttaccctac 1926
 237 AAAAGCTCTGCTCAATCCCAACGACTTTGTGAGCGCGGGTCCAGAGCTGGGTAT 296
 1927 accaatctctgcctccgagcagacctgagcccgccgctcgtctatccccaactac 1986
 QY 297 TATTTCCGTGATGACAGCCTGCGGTGTGACGCGATGAGAGGTACGTGACTAGAGAT 356
 1987 cactaccgagagcagcgagcctgagatctgagcgccatgagagccttgcctcagaatc 2046
 QY 357 CATCATTATTTATTCACCAATGAC 380
 2047 gtgggctactattatcccaagtgac 2070

RESULT 8
 AAC61758
 ID AAC61758 standard; cDNA; 2604 BP.

XX AAC61758;

XX 06-MAR-2001 (first entry)

XX cDNA encoding a human lipoxigenase protein.

XX Human; lipoxigenase; leukotriene; lipid; chemotactic agent;
 KW inflammation; smooth muscle contraction; asthma; eye disease; arthritis;
 KW lung disease; cancer; acne; psoriasis; ss.

Homo sapiens.
 Key Location/Qualifiers
 CDS 1..2604
 /*tag= a
 /product= "lipoxigenase"

MO200061765-A2.

19-OCT-2000.

12-APR-2000; 2000MO-US09657.

12-APR-1999; 99US-0128817.

24-AUG-1999; 99US-0150454.

(LEXI-) LEXICON GENETICS INC.

Turner CA, Zambrowicz B, Nehls M, Friedrich G, Sands AT;

WPI: 2000-665134/64.

P-PSDB; AAB19390.

Novel polynucleotides encoding human lipoxigenase proteins useful for producing transgenic animals preferably mouse
 Claim 1; Page 73-74; 83pp; English.

AAC61747-60 encode novel human lipoxigenase proteins. Lipoxigenases oxidise lipids to produce leukotrienes. Leukotrienes bind cognate receptors and trigger biological effects. Leukotrienes influence a variety of biological processes, and can serve as, inter alia, potent chemotactic agents and mediators of inflammation, smooth muscle contractions, etc.. Lipoxigenases and leukotrienes are implicated in a variety of diseases and disorders, such as asthma, eye diseases, arthritis, lung disease, cancer, acne, psoriasis, etc..

Sequence 2604 BP; 554 A; 840 C; 709 G; 501 T; 0 other;

Query Match 14.5%; Score 55.2; DB 21; Length 2604;
 Best Local Similarity 54.4%; Pred. No. 1.4e-07;

Matches 111; Conservative 0; Mismatches 93; Indels 0; Gaps 0;

QY 177 TCCCTGGGCTAGAGGCTTGCACAGGTGATGGTTCGGGTCTGTGAGCTACCTAC 236
 1867 tccatcgaggaagagcctcatctactatgagcaagcgccgcccacttaccctac 1926
 237 AAAAGCTCTGCTCAATCCCAACGACTTTGTGAGCGCGGGTCCAGAGCTGGGTAT 296
 1927 accaatctctgcctccgagcagacctgagcccgccgctcgtctatccccaactac 1986
 QY 297 TATTTCCGTGATGACAGCCTGCGGTGTGACGCGATGAGAGGTACGTGACTAGAGAT 356
 1987 cactaccgagagcagcgagcctgagatctgagcgccatgagagccttgcctcagaatc 2046
 QY 357 CATCATTATTTATTCACCAATGAC 380
 2047 gtgggctactattatcccaagtgac 2070

RESULT 9
 AAC61747
 ID AAC61747 standard; cDNA; 2701 BP.

XX AAC61747;

XX 06-MAR-2001 (first entry)

XX cDNA encoding a human lipoxigenase protein.

XX Human; lipoxigenase; leukotriene; lipid; chemotactic agent;
 KW inflammation; smooth muscle contraction; asthma; eye disease; arthritis;

KW	Lung disease; cancer; acne; psoriasis; SS.
OS	Homo sapiens.
XX	
XX	
FT	Key location/Qualifiers
FT	CDS 1..2136
FT	/tag= a
FT	/product= "lipoxygenase"
XX	
PX	
PA	WO20061765-A2.
PD	19-OCT-2000.
XX	
PF	12-APR-2000; 2000WO-US09657.
PR	12-APR-1999; 99US-0128817.
PR	24-AUG-1999; 99US-0150454.
XX	
PI	(LEXI-) LEXICON GENETICS INC.
PI	Turner CA, Zambrowicz B, Nehls M, Friedrich G, Sands AT,
DR	WPI, 2000-665134/64.
PT	P-PDB; AAB19379.
PT	Novel polynucleotides encoding human lipoxygenase proteins useful for
XX	producing transgenic animals preferably mouse .
PS	Claim 1: Page 57-58; 83pp; English.
XX	
CC	AAC61747-60 encode novel human lipoxygenase proteins. Lipoxygenases
CC	oxidise lipids to produce leukotrienes. Leukotrienes bind cognate
CC	receptors and trigger biological effects. Leukotrienes influence a
CC	variety of biological processes, and can serve as, inter alia, potent
CC	chemoattractants, etc.. Lipoxygenases and leukotrienes are implicated in
CC	contractile agents, etc.. Lipoxygenases and leukotrienes are implicated in
CC	a variety of diseases and disorders, such as asthma, eye diseases,
CC	arthritis, lung disease, cancer, acne, psoriasis, etc..
XX	
SO	Sequence 2701 BP; 588 A; 869 C; 690 G; 554 T; 0 other;
Oy	Query Match 14.5%; Score 55.2; DB 21; Length 2701;
	Best Local Similarity 54.4%; Pred. No. 1.4e-07;
	Matches 111; Conservative 0; Mismatches 93; Indels 0; Gaps 0;
Dy	177 TCCCGGGGCGGTAGAGGGGCTGCACAGGTATGTTGGGGTCTGTCGTGACTCACCTAC 236
	1399 tccatcgaggagcgaacgcttactctactctactgatgcagcgccgtcccttcacctac 1458
	237 AAAAGCCTCTGCATTCCCAACGACTTCTTGAGCGGGGCMCAAGACCTGCCGGGTAT 296
Dy	1459 accaatctctcctccgccgagacagcttgccggccgcgcgcgtcgtctaccctaac 1518
Oy	297 TATTTCTCGATGACAGCGCTGCGGTGTGTACCGCATGGAGAGTAAGTACAGAT 356
Dy	1519 cactaccgagacgacgctgaagaatctggcgcccatltgagagacttgtctcaagaatc 1578
Oy	357 CATCACTTATTATTACCAAATGAC 380
Dy	1579 gtgggctactattatcccagttac 1602
RESULT 10	
ID	ABA05868
XX	ABA05868 standard; CDNA; 3320 BP.
XX	ABA05868;
AC	
XX	
DT	21-MAR-2002 (first entry)
XX	
DE	Human lipoxygenase 46638 coding sequence.
XX	

```

XX OS Homo sapiens.
XX EH Key location/Qualifiers
XX FT CDS 459..2594
XX FT /*tag=
XX FT /*product= "lipoxygenase 46638"
XX FT /note= "this region is specifically claimed"
XX PN WO200190323-A2.
XX PD 29-NOV-2001.
XX PF 21-MAY-2001: 2001WO-US16380.
XX PR 19-MAY-2000: 2000US-205675P.
XX PA (MILL-) MILLENNIUM PHARM INC.
XX PA Meyers RA;
XX PT WPI: 2002-083104/11.
XX DR P-PSDB; ABB04578.
XX DX
XX PT Novel human lipoxygenase family member polypeptide and polynucleotide
XX PT for diagnosing, treating immune, blood vessel, cardiovascular,
XX PT inflammatory, ovarian, lung, colon, skin disorders and disorders
XX PT involving placenta -
XX PT
XX PT Claim 1: Page 100-102; 118pp; English.
XX
XX XX The present invention provides the protein and coding sequences of a
XX CC human protein, which is a member of lipoxygenase family, and is referred
XX CC to as 46638. The sequences can be used in the treatment of immune, blood
XX CC vessels, cardiovascular, inflammatory, cell differentiation,
XX CC neurodegenerative, liver, ovarian, lung, colon, breast, skin disorders,
XX CC disorders associated with bone metabolism, pain or metabolic disorders,
XX CC disorders involving the placenta and viral diseases. The present sequence
XX CC is the coding sequence of the invention.
XX CC
XX CC Sequence 3320 BP; 706 A; 1074 C; 852 G; 683 T; 5 other:
XX CC
XX CC Query Match 14.5%; Score 55.2; DB 24; Length 3320;
XX CC Best Local Similarity 54.4%; Pred. No. 1.6e-07;
XX CC Matches 111; Conservative 0; Mismatches 93; Indels 0; Gaps 0.
XX
XX 177 TCCCTGGGCTCAGAGGCTTCGCACAGGTGATGCTGGGGTCTGTCGTGAGCTCAGCTAC 236
XX ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
XX DB 1857 tccatcggaagcaagagcctcatcatcatcattagagcagcgccctgagcccactcaccctac 1916
XX
XX 237 AAAACCTCTGCATTTCCCAAGAGCTTTGTGGAGCGGGGTCTGCAGACCTGCCTGGGGTAT 296
XX ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
XX DB 1917 accaatcttcgtcctcggaagagcctcgcgagcccgcgctcctcggtatccccaactac 1976
XX
XX 297 TATTTCGCGATGACAGCGCTGGCGGTTGTGTAGCCGATGACAGAGCTACGTGACTAGAGAT 356
XX ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
XX DB 1977 cactacagagagcagcgctcgagaatcgtgagcgagcaltgagagcttcttcagaatc 2036
XX
XX 357 CATCACTATTATTTCACCAATGAC 380
XX ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
XX DB 2037 gtgggtactactatcaccagtgac 2060
XX
XX RESULT 11

```

XX	25-JUN-1999	(first entry)
XX		
DE	Human 15S lipoxygenase PS213 DNA.	
XX		
KW	Lipoxygenase; PS213; human; diagnosis; prostate disease; cancer;	
KW	metastases; benign prostatic hypertrophy; prostatic; immunosay;	
KW	prostatic intraepithelial neoplasia; cytotoxic agent; drug screening;	
XX	therapy; ss.	
OS	Homo sapiens.	
XX		
XX	WO913111-A1.	
XX		
PD	18-MAR-1999.	
XX		
PF	11-SEP-1998; 98MO-US18983.	
XX		
PR	11-SEP-1997; 97US-0927978.	
XX		
PA	(ABBO) ABBOTT LAB.	
XX		
PI	Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN;	
PI	Gordon J, Granados EN, Hodges SC, Klass MR, Kratochvil JD;	
PI	Russell JC, Stroupe SD;	
DR	WPI: 1999-229254/19.	
DR	P-PSDB: AAW93832.	
XX		
PT	Diagnosis of prostatic disease using lipoxygenase PS213 as marker	
XX		
XX	Claim 1; Page 93; 101pp: English.	
XX		
CC	This invention describes methods for diagnosing prostate disease using	
CC	the human 15S-lipoxygenase PS213, or its nucleic acid or specific	
CC	antibodies, as markers. Detecting the presence of PS213, a derived	
CC	amplicon, the encoded polypeptide or specific antibody, basically in	
CC	standard hybridization, amplification or immuno assays, indicates	
CC	prostatic disease. These methods are used for diagnosis, staging,	
CC	monitoring, prognosticating, in vivo imaging and determining	
CC	predisposition to prostatic cancer (and metastases), benign prostatic	
CC	hyper trophy, prostatic, and prostatic intraepithelial neoplasia. Host	
CC	cells transfectd with PS213 are used to produce recombinant	
CC	polypeptides which are used to generate antibodies or as immunoassay	
CC	reagents. The antibodies, and their fragments, are also immunoassay	
CC	readants and can be used therapeutically, either directly or as carriers	
CC	for cytotoxic agents. The recombinant polypeptides are also used for	
CC	drug screening and as targets for therapy.	
XX		
SO	Sequence 2647 BP; 591 A; 828 C; 721 G; 507 T; 0 other;	
Query Match	13.2%; Score 50; DB 20; Length 2647;	
Best Local Similarity	56.6%; Pred. No. 7 le-06;	
Matches 112; Conservative	0; Mismatches 85; Indels 1; Gaps	
QY	179 CCTGGGCTTAAGAGGCTTTCGCACAGGTAGTTCGGGGCTGTCTGAGCTCACTACAA	238
DB	1367 catcggaattgaagagctctctcttgattgatacagagaaacatgaacagctgaactatc	1426
QY	239 AAGCGTGCATTTCCCAACGACTTTGTGGAGCGCGGGGTCACAGACTCGTGGGATTA	298
DB	1427 tctctgtgtctgcttgagagataatccgagccgaggaagttaagaacatcccgagcttacc	1486
QY	299 TTTCCGATGATGACAGCTGCGCGGTGTGATACGGATGAGAGAGTACGTACTAGAGATCA	358
DB	1487 ctacagtgatgatgtgagttgcagatttgagggtgcagtggaacgtttgtctc-gaatca	1545
QY	359 TCACTTATTATACCAA 376	
DB	1546 tcggtatctactactaccacaa 1563	

RESULT 13

AAD04501 standard; cDNA; 2685 BP.

ID AAD04501;

04-JUL-2001 (first entry)

Human 15S-lipoxygenase (15-Lox-2) cDNA.

Human; 15S-lipoxygenase; 15-Lox-2; non-haeme iron dioxxygenase; arachidonic acid; feed additive; livestock; antigen; ss.

Homo sapiens.

Key	Location/Qualifiers
CDS	72..2102
	/tag= a
	/product= "Human 15S-lipoxygenase (15-Lox-2) protein"

US6204037-B1.

20-MAR-2001.

16-APR-1998; 98US-0061768.

16-APR-1998; 98US-0061768.

(UYVA-) UNIV VANDERBILT.

Brash AR, Boeglin WE, Jisaka M;

WPI; 2001-289517/30.

P-PSDB; AAE00935.

New 15S-lipoxygenase nucleic acids and polypeptides, useful as feed additives for livestock, or as antigens for producing antibodies -

Claim 3; Column 43-48; 51pp; English.

The present sequence is human 15S-lipoxygenase (15-Lox-2) cDNA. Lipoxygenases are a structurally related family of non-haeme iron dioxxygenases that function in the production of fatty acid hydroperoxides. 15-Lox-2 acts in the metabolism of arachidonic acid to 15-hydro(pero)xyicosatetraenoic acid. Lipoxygenase DNA can be used as diagnostic tools to detect normal and abnormal DNA sequences derived from patient cells, for detecting and isolating other members of the polypeptide family and related polypeptides from a DNA library potentially containing the sequences, as primers for hybridizing to related sequences for amplifying those sequences or for altering native lipoxygenase DNA sequences. The lipoxygenase is useful as feed additives for livestock and as antigens for producing antibodies.

Sequence 2685 BP; 625 A; 829 C; 721 G; 510 T; 0 other;

Query Match 13.2%; Score 50; DB 22; Length 2685;

Best Local Similarity 56.6%; Pred. No. 7.1e-06; Matches 112; Conservative 0; Mismatches 85; Indels 1; Gaps 1;

179 CCGGCGCTAGAGGCTTCGCACAGGTGATGTTCCGGGCTCTGCTGACCTGACCAACA 238

1367 catcgatgaaagctctctcgtgatacagaagaacatgaagcagctgaactatc 1426

239 AAGCTCTGCACTCCCAACGACTTGTGAGAGCGGGCTCCAGGACCTGCGGTATTA 298

1427 tctcctggtctccttaagatacccgaccgagaggttgaagaactccacagctacta 1486

299 TTTCCTGATGACAGCCTGCGGCTGTGATACGAGTGAAGAGTACTGATGACAGATCA 358

1487 ctacgcgatgatgagatgcagatttggtggtgagtgagaaagcttctcct- gaataca 1545

OY 359 TCACCTATTATTACCAAA 376

DB 1546 tcggtatctactaccaca 1563

RESULT 14

AAD04502 standard; cDNA; 3232 BP.

ID AAD04502;

04-JUL-2001 (first entry)

Mouse 8S-lipoxygenase (8-Lox) cDNA.

Mouse; 8S-lipoxygenase; 8-Lox; non-haeme iron dioxxygenase; arachidonic acid; feed additive; livestock; antigen; ss.

Mus sp.

Key	Location/Qualifiers
5'UTR	1..27
	/tag= a
CDS	28..2061
	/tag= b
	/product= "Mouse 8S-lipoxygenase (8-Lox) protein"

US6204037-B1.

20-MAR-2001.

16-APR-1998; 98US-0061768.

16-APR-1998; 98US-0061768.

(UYVA-) UNIV VANDERBILT.

Brash AR, Boeglin WE, Jisaka M;

WPI; 2001-289517/30.

P-PSDB; AAE00936.

New 15S-lipoxygenase nucleic acids and polypeptides, useful as feed additives for livestock, or as antigens for producing antibodies -

Example 2; Fig 5A-5C; 51pp; English.

The present sequence is mouse 8S-lipoxygenase (8-Lox) cDNA. Lipoxygenases are a structurally related family of non-haeme iron dioxxygenases that function in the production of fatty acid hydroperoxides. 8-Lox acts in the metabolism of arachidonic acid to 8S-hydro(pero)xyicosatetraenoic acid. Lipoxygenase DNA can be used as diagnostic tools to detect normal and abnormal DNA sequences derived from patient cells, for detecting and isolating other members of the polypeptide family and related polypeptides from a DNA library potentially containing the sequences, as primers for hybridizing to related sequences for amplifying those sequences or for altering native lipoxygenase DNA sequences. The lipoxygenase is useful as feed additives for livestock and as antigens for producing antibodies.

Note: The present sequence is also shown in column 51-58 of the specification, but lacks 27 nucleotides at its 5' end.

Sequence 3232 BP; 823 A; 872 C; 782 G; 755 T; 0 other;

Query Match 13.2%; Score 50; DB 22; Length 3232;

Best Local Similarity 53.0%; Pred. No. 7.7e-06; Matches 107; Conservative 0; Mismatches 95; Indels 0; Gaps 0;

179 CCGGCGCTAGAGGCTTCGCACAGGTGATGTTCCGGGCTCTGCTGACCTGACCAACA 238

1326 ccttgcactgggggactctcgtacctgataaagaagaacatggagcagctgaactactc 1385

Search completed: May 25, 2002, 01:31:09
Job time: 5743 sec

